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Sent:

Helmer, Georgia Monday, July 29, 2002 10:59 AM STIC-Biotech/ChemLib

To: Subject:

09/643,755

Could you please do sequence searches of SEQ ID 1, 2, and 3 of this case, 09/643,755.

SEQ ID 1 and 3 are DNA. SEQ ID 2 is protein.

Could you also do an oligo search of SEQ ID 1 and 3.

The commercial and inhouse databases.

Thanks in advance for you assistance.

Georgia L. Helmer Rh.D. Patent Examiner Crystal Mall 1, 9D14 **AÚ 1638** 703-308-7023 Georgia.Helmer@USPTO.gov mailbox 9e12

GMMS G1.

**Point of Contact: Toby Port** Technical Info. Specialist CM1 6A04 703-308-3534

Searcher: Phone: \_ Location: Date Picked Up: \_ Date Completed: \_ Searcher Prep/Review: \_ Clerical: Online time: \_

TYPE OF SEARCH:	
NA Sequences:	
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Other:	

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: \_\_\_ DRLink: \_ Lexis/Nexis: \_ Sequence Sys.: \_ WWW/Internet: Other (specify):

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## ALIGNMENTS

CDS	source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX088019	RESULT 1
/organism="Bos taurus" /db_xref="taxon:9913" 1. 1173 /note="unnamed protein product"	11173	Location/Qualifiers	Patent: WO 0114571-A 1 01-MAR-2001;	Commercial production of chymosin in plants	van Rooijen, G., Keon, R.G., Boothe, J. and Shen, Y.	1 (bases 1 to 1173)	Bovidae; Bovinae; Bos.	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bos taurus	COW.		AX088019.1 GI:13396947	AX088019	Sequence 1 from Patent WO0114571.	AX088019 1173 bp DNA linear PAT 17-MAR-2001		

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                                                                                                                ATCTTGGATACCGGTACGTCCAAGCTGGTCGGACCTAGCAGCGACATTCTCAACATTCAG
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J00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chymosin is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically different forms, a and b, of the enzyme and its precursor are known and a third form seems likely (see boychymoa, boychymoc). this sequence has tentatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H. molecular cloning and nucleotide sequence of cdn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bo
1 (bases 1 to 1305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                been identified as coding for preprochymosin b. sequence comparison indicates that the precursors for chymosins a and b differ by only two amino acids, and for b and c by only four amino acids.
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bovine (calf) cdna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAA30448.1"
/db_xref="GI:162860"
/td_xref="GI:162860"
/translation="MRCLVVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
QKQQYGISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDEWVPS
IYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
<1. .1305</pre>
                                                                                                                                                                                                                                                                                                                                              /product="chymosin 393 c 340 g
                                                                                                                                                                                                                                                                                                                                                                                /note="presequence" 200. .1168
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26. .1171
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87.8%;
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Cetartiodactyla;
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Pred. No. 5e-263;
0; Mismatches 136;
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fourth stomach mucosa
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actyla; Ruminantia;
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Sequence 2 :
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AR002347.1
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Unclassi
l (base
Kato, E.K
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Stuart, W. Dorsey
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                              aagctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaaca
                         AGGCCATCCTGGACACGGGCACCTCCAAGCTGGTCGGGCCCAGCAGCGACATCCTCAACA
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980; Conserv
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nilarity 87.7%;
Conservative
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374 c 339 g
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Location/Qualifiers
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Pred. No. 4.7e-262;
0; Mismatches 138;
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DNA coding of pre-pro
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E00042.1 GI:2168348
JP 1982141287-A/1.
unidentified.
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1/00,C07G7/00,C07H21/04,C12N15/00,C12P21/00//C12N1/18,
      a
    /organism="unidentified"
/db_xref="taxon:32644"
440 c 398 g 29
                             Location/Qualifiers
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                           cctccgcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaacc
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                                                                                 ACCTGAGCTACATGCCCACTGTGGTCTTTGAGATCAATGGCAAAATGTACCCACTGACCC
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Pred. No. 4.7e-262;
0; Mismatches 138;
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chymosin d
A15836
A15836.1
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1 (bases 1 to 1291)
Simons, A.F.M. and De Vos, W.M.
DNA fragments, containing a lactic a
DNA fragment for the expression
regulator region for the expression
                                                                                                                                                                                                                                                                                                                                                                                                  cow.
Bos taurus
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Mammalia; I
                                                                                                                                                                                                                                                                                                                      heterologous proteins
Patent: EP 0307011-A 5 15-MAR-1989;
NEDERLANDS INSTITUUT VOOR ZUIVELONDERZOEK
Location/Qualifiers
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                                                                                                                                                                                                                                                    Conservative
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/db_xref="taxon:9913"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                          76.4%;
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Pred. No. 9.5e-262;
0; Mismatches 139;
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activity
Patent: E
                                                                                                                                                   Sequence
104058
104058.1
                                                                                                      Unclassified.

1 (bases 1 to 1175)
Cashion,L.M., McCaman,M.T., Rice,C.W. and Recombinant DNA coding for a polypeptide of
                                                                                                                                 Unknown
                                                                                                                                       Unknown
                                                                                                                                                                       I04058
                                Similarity
                          Conservative
                                                                 а
                                                                                          EP 0123928-A2 5 07-NOV-1984;
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                                                                            Location/Qualifiers
                                                                 /organism="unknown"
356 c 318 g
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87.6%;
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Pred. No. 1.4e-261;
0; Mismatches 139;
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EP 0123928.
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                                           tgttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggagctattg
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Unclassified.

1 (bases 1 to 2733)

1 (bases 1 to 2733)

Moloney,M.M.

Preparation of heterologous proteins on the proteins on the proteins on the protein of the
ttcgatggcatccttggtatggcatacccatcgctcgcgtcagagtactcgatacctgtg
                                                                                                                                                                                                                                                                                                                                                         TTCGACGGGATCCTGGGGATGGCCTACCCCTCGCCTCAGAGTACTCGATACCCGTG
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Unknown.
Unclassifi
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Similarity 88.4%;
71; Conservative
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Pred. No. 2.7e
0; Mismatches
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5948682
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2.7e-261;
ches 127;
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VERSION
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 sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctagctaaagcaatctga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATCAGCGGTGTGGTGGGCCTGTGAGGGTGGCTGTCAGGCCATCTTGGACACGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOVCHYMOA
bovine chy
J00002
                                                                                                                                                                                                                                                                                                                                                                                            J00002.1 GI:162857
chymosin; chymosin A; rennin.
bovine (calf) cdna of fourth s
Bos taurus
Busaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                     chymosin (rennin) is the major proteolytic enzyme in the fourth stomach of the unweaned calf, two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymoc), this sequence has been tentatively identified as chymosin a; it differs from chymosin b by only two amino acids from chymosin c by another amino acid. [1] argues that the
                                                                                                                                                                                                                                                                                                   molecular cloning and characterization coding for bovine chymosin Gene 19, 127-138 (1982)
                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
1 (bases 1 to 1275)
Moir.D., Mao.J.I., Schumm,J.W.,
Taunton-Rigby,A.
                                                                                                                                                                                                             different chymosins
                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          m∪A
chymosin a (rennin) mrna.
VGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRN GQESMLTLGAIDFCYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTG TSKLVGPSSDILNIQQAIGATQNQYDEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT SQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI" 24. . 68
                                                         /codon_start=1
/protein_id="AA30447.1"
/protein_id="AA30447.1"
/db_xref="GI:162858"
/translation="MRCLVVLLAVFALSQGAETTRIPLYKGKSLRKALKEHGLLEDFL
/KRONGISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPS
IYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNILDIQQT
                                                                                                                                                                                                  gene
                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                            /note="preprochymosin
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1173
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                                                                                                                                                                                                          are probably polymorphic
                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebra:
Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                     rennin.
fourth stomach
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T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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minantia; Pecora;
                                                                                                                                                                                                                                                                                                                              double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                      mrna.
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                                                                                                                                                                                                             variants of
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Query Match
Best Local S
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                                                                                                                                                         CTGTCTCCAACATTCTCGACATCCAGCAGACAGTAGGCCTGAGCACCCAGGAGCCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTCGCTCTCCCCAGGGCGCTGAGATCACCAGGATCCCTCTGTACAAAGGCAAGTCTC 108
                                                                                                 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggagctattg
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                                                       ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
                                                                                                                                                                                                                   TCCAGCAGGCCATTGGAGCCACACAGAACCAGTACGATGAGTTTGACATCGACTGCGACA
                                                                                                                                                                                                                                                                           TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCTGGGGGGCCATCG
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978; Conser
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nilarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 894; DB
Pred. No. 4.4e-
0; Mismatches
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No. 4.4e-261;
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REFERENCE
AUTHORS
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VERSION
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SOURCE
ORGANISM
              δõ
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LOCUS
DEFINITION
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JOURNAL
                                    Query Match 76.2%;
Best Local Similarity 87.5%;
Matches 978; Conservative
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              56
                                                                                                                                                                PRODUCTION OF POLYPEPTIDE
PRODUCTION OF POLYPEPTIDE
AL Patent: JP 1983009687-A.1 20-JAN-1983;

CELLTECH LTD
OS bovine
OS bovine
PN JP 1983009687-A.1
PD 20-JAN-1983
PF 17-UN-1981 GB 81 8118688, 11-NOV-1981 GB 81 81
01-DEC-1981 GB 81 8136185, 10-FEB-1982 GB 82 820390;

NOMAN HENRI KEARI, MAIKERU TERENSU DOORU,
PI CHLMOSHII JIYON ROI HARISU,
PI CHLMOSHII ROU, JIYON SUPENSAA EMUTEEJI
PC C12N9/52,C07H21/04,C12N1/00,C12N9/60,C12N15/00, PC
C12R1/865;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC *SOUTCE: tissue_type=stomach;
CC *SOUTCE: tissue_type=stomach;
CC *SOUTCE: clone=pCT 70;
FH Key Location/Qualifiers
FH FY 5'UTR
FT 5'UTR
FT 5'UTR
FT 3'UTR
1081
PT c1081
PT CDS 26. 1081
FT CDS 26. 1081
PT CDS 26. 1081
tcgttgctgttactcacgctgctgagatcacccgcattcctctctacaaaggtaagtctc
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CDNA encoding chymosis

E00075

E00075.1 GI:2168379

JP 1983009687-A/1.

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Nooman, H.K., Maikeru, T.D.,
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                                                                                                        /product='pre-pro-chymosin'
1.ocation/Qualifiers
1.oration/Qualifiers
                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
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                                  Score 894; DB 6; Pred. No. 4.4e-261; O; Mismatches 140;
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1 (bases 1 to 1291)
Carey,N.H., Doel,M.T., Harris,T.J.R., Lowe,P.F.
A process for the production of a polypeptide
Patent: EP 0068691-A 29 05-JAN-1983;
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/protein_id="CAA01244.1"
/protein_id="CAA01244.1"
/db_xref="G1:491952"
/db_xref="RECLYVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
/trans1atlon="NRCLYVLLAVFALSQGAEITRIPLYKGKSSLFWPS-
RKQQYGISSKYSGFGEVASYPFLTYLLDSQYFGKIYLGTPPGPETYVLFDTGSSDFWPS-
IYCKSNACKHHQRFDPRKSSTFONLGKPLEIHYGTGSMQGILGYDTYTVSNIVDIQQT
VGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRI
GDESMLTLGAINPSYYTGSLHWVPVTVQOYMQFTVDSVTISGVVVVACEGGQAILDTG
TSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT
SODOGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
1291
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/db_xref="taxon:32630"
26. .1171
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Patent: JP 1984021392-A 1 03-FEB-1984;

GENEX CORP
OS bovine calf
S bovine calf
PN JP 1984021392-A/1
PD 03-FEB-1984
PF 30-JUN-1983 JP 1983119481
PF 30-JUN-1982 US 82 394433, 13-APR-1983 US 83
CHIVAARUSU EI BASUBETSUTO
PC C12N15/00,C07H21/04,C12N1/20,C12P19/34,C12P21/02,(PC C12R1:19);
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JP 1984021392-A/1.
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388 c 329 g 26
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                                      GGACAGTCAGTACTTTGGGAAGATCTACCTCGGGACCCCGCCCCAGGAGTTCACCGTGCT
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Sequence
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DNA constructs containing a Kluyveromyces alpha-
sequence for directing secretion of heterologous
Patent: EP 0301669-A1 5 01-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                   Unclassified
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RECOMBINED DNA
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PD 29-JUN-1983
PF 14-OCT-1982 JP 1982180549
PR 14-OCT-1981 GB 81 8131004
PI YAN MAATO, KORUNEERISU SEDDORUSU BERURITSUPUSU, PI ADORIANUSU MARINUSU REDEBOERU, RUTSUPO EDENSU PC CO7H21/04,C12M1/20,C12M15/00//C12P21/00;
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC *Source: tissue_type=stomach;
FH Key Location/Qualifiers
FH Key /product='prepro chymosin'
FT sig_peptide 24..1169
FT sig_peptide 72..1166
FT mat_peptide 72..1166
FT mat_peptide 72..1166
FT mat_peptide 198..1166
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 cagagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagact
                                                                                                   ctgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtg
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                                                                                                                                           CCCTGTCTATCCACTACGGGACACGCAGCATGCAGGGCATCCTGGGCTATGACACCGTCA
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/db_xref="taxon:32644"
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Pred. No. 1.4e-260;
0; Mismatches 141;
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Debuitsudo, B., Jien, I. M., Donarudo, T. M., Arison, T.R.,
Robaato, J. N., Jien, I. M., Donarudo, T. M. and Kurisutofuaa, G. G.
USE OF GAL YEAST PROMOTOR
USE OF GAL YEAST PROMOTOR
Patent: JP 1985058077-A 3 04-APR-1985;
KORABDRATEIBU RES INC
S BOVINE
PN JP 1985058077-A/3
PD 04-APR-1985
PF 28-FEB-1984 JP 1984035472
PR 28-FEB-1984 JP 1984035472
PR 28-FEB-1983 US 83 470911
PI DEBUITSUDO BOTSUTOSUTEIN, RONARUDO UEIN DEIBUISU, PI
JIERARUDO RARUFU RIGUBII, ROBAATO JIENTORII NOURUTON, JIEN I
MAO, PI DONARUDO TEIRAA MOA, KURISUTOFUAA GOTSUDOFURII GOFU PC
C12N15/00,C07H21/04,C07K13/00,C12N1/16,C12P21/02,(C12N1/16, PC
C12R1-865);
CC c12P21/02,C12R1:865);
CC strandedness: Double;
CC copology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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E00295
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                                                                                                                                                                                                                                                          Bos taurus
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977; Conserv
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*source: clone=293-207 & 293-118/37;
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/db_xref="taxon:9913"
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87.48;
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205...1347
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Pred. No. 1.4e-260;
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Search completed: July 31, 2002, 18:18:54 Job time: 20085 sec

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         0 00 ~1 00 01 <del>4</del> 00 01
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Copyright (c) 1993 - 2000 Comp
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## ALIGNMENTS

RESULT AAS00569 Bovine pre-pro-chymosin DNA sequence. 14-MAY-2001 AAS00569 standard; DNA; 1173 BP (first entry)

Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds. mat\_peptide misc\_feature CDS Bos sig\_peptide qs. /product= '
1..78 /\*tag= c /note= "Pro: 202..1170 /\*tag= 79..201 /product= Location/Qualifiers
1..1173 ٦ "Mature bovine chymosin" "Bovine chymosin" sequence"

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pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant; French bean.
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                                                                          precursor_RNA
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                                                                                                                    acid
                                                                                                                                        sequence
                                                                                                                                                                                                         standard;
                                                                                                         pSK112;
                                                                                                                  bacteria; cheese;
                                                                                                                                                             (first
                                                                                                                                       of (pro)chymosin
                                                                         Location/Qualifiers 29..1123
                                                    /product=;prochymosin
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                                                                                                                                                                                                        DNA;
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                                                                                                                                                            entry)
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                                                                                                                    Streptococcus
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA fragment having region specific for lactic acid bacteria is contained in plasmid in microorganism used in prodn. of protein and food prodn. eg cheese.
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                                            cagagtactcgatacctgtgttttgacaacatgatgaaccgacacctagtagctcaagact
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                                cagagtactcgatacccgtgtttgacaacatgatgaacaggcacctggtggcccaagacc
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       expressed
                Recombinant DNA coding
                                 P-PSDB;
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       nt DNA coding for milk clotting in transformed bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Local Similarity 68.2%; P
nes 763; Conservative 217;
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                                                                                                                                                                                                                    ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca: ||||| || ||::||||: || :||||||
                                             atccatcctactacacaggatctcttcactgggttccagtcactgtgcagcagtactggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 897.2; DB 5;
Pred. No. 7e-273;
L7; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
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RESULT AATTO3006 TO AATTO3006 AATTO3
                                                    The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological status of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic
albino p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
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gene; expression; control; chymosin;
  B₽;
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entous fungi
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Query Match Best Local S Matches 980

Similarity

76.5%; 87.7%;

Score 897.2; I Pred. No. 7.2e 0; Mismatches

.2e-273;

DB 16;

Length

1240; 0;

Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a DNA segment contg. GAL1 promoter linked to gene - useful for direction of expression of the gene in yeast or the recombinant material carrying a GAL1 promoter of the yeast galactokinase gene may be used in expressing a desired protein, bovine growth hormone, interferon, prorennin or preprorennin, in yeast cell. Strains of Saccharomyces cerevisiae producing the polypeptides are produced. Yeast strains deposited as ATCC 20643 20661, 20662 and 20663, strain designations CGY 196, 457, 461 an 528, resp. are new.
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milk-clotting
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Location/Qualifiers
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be removed and are not essential to use of the gene expression. The gene may be ligated into plasmid pcGE21 expressed in E. coli. The resulting expressed enzyume is known milk-clotting enzyme used in cheese-making
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformed
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16-JAN-1981;
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ccctgtctatccactacgggacaggcagcatgcagggcatcctgggctatgacaccgtca
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/note= "CDS
850..1202
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1203..1442
/number= 1
1443..2733
                                                                                                                                                                                            body; oleosor
heterologous
                                                                                                                                   Location/Qualifiers 850..2729
                                                                                                                                                                                                                         fragment of psbsotptnt
                                                                                                                                                                                                                                                                                     DNA;
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                                                                                                    "oleosin-spacer-Met-prochymos
DS contains an intron"
                                                                                                                                                                                            polypeptide;
                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                      spherosome;
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25-APR-1997;
22-FEB-1991;
16-NOV-1993;
30-DEC-1994;
                        proteins, thrombin inhibitors, hirudin, interleukins, chyn xylanase, carp growth hormone, zein or a collagenase. The enzyme may be cleaved from the oil body protein or use association with the oil body fraction. Allows production of commercially important proteins on a to production by conventional systems. The expressed heter protein can be easily separated from host cell components due to the use of the oil body as a carrier protein.
                                                                                                                                                   B napus plants.

The DNA which encodes a chimeric fusion protein that consists of oil-body trargeting sequence, a transcription regulation sequence DNA of the protein of interest can be used to produce antibodies, proteases, protease inhibitors, seed storagelycanases, hormones, proteases, protease inhibitors, seed storagelycanases.
                                                                                                                                                                                                                                   This is the nucleotide sequence of a HindIII fragment containing the oleosin-spacer-Met-prochymosin sequence. This HindIII fragment was joined to a nopaline synthase terminator and cloned into binary vector pCGN1559. The resulting plasmid was called pSBSOTPTNT and introduced into A.tumefaciens. The resulting bacterial strain was used to transform
Sequence
                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                              Expression of a heterologous useful for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moloney
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DB; AAY33830.
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BP;
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91US-0659835.
93US-0142418.
94US-0366783.
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699
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681 C;
                                                                                                                                                                                                                                                                                                                                                               polypeptide on an oil body protein e.g. enzymes, antibodies, hormones
684 G;
669
T; 0 other;
                                                                                                          or used
                                                           on a superion heterologous
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                                   gatcogagaaagtcgtccaccttccagaacttaggcaaacccttgtctatacactacggt
                                                                        gacttotgggttocototatotactgcaagagcaatgcotgcaagaaccaccaaagatto
                                                                                                            aagatctacctcggaaccccgctcaagagttcaccgttctctttgatactggttcctct
                                                             gacttctgggtaccctctatctactgcaagagcaatgcctgcaaaaaccaccagcgcttc
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0; Mismatches
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5.3e-272;
hes 127;
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RESULT ID AAQ14051
AAQ14051
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AC AAQ
XX Pro
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XX BPO 16--
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11-APR-1990;
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                                                       16-0CT-1991
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90DE-4011751
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Recombinant DNA constructs for expressing protein in milk -
contg. specific mammary gland transcription control region and
signal sequence, providing high yield and easy prod. recovery
                                                                                  Disclosure;
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                                                                                                                                                                    CONSORT ELEKTROCHEM
                                                                                  Page 21;
                                                                                 41pp; German.
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It was used as heterologous peptide/protein together with parts of the alpha-S1-casein gene in the prodn. of DNA constructs. The heterologous peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland See also AAQ14050, AAQ14774-77. heterologous

Sequence 1210 BP; 278 Α; 356 C; 324 ر. ق 252 H 0 other;

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P-PSDB; AAP30446.
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alf stomach chymosin of micro-organisms
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Matches
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ВP

veal chymosin

zymogen; rennin; chymosin; cheese making;

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Best Local Similarity
Matches 975; Conserv
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01-JUL-1982;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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ctgtctccaacattgtggacatccagcagacagtaggcctgagcacccaggagcccgggg
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Copyright (c) 1993 - 2000 Compugen Ltd
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A1326975 mj81e03.x
BG937723 1Abo05D06
AK004109 Mus muscu
BG938086 1Abo11A08
AA028632 mi14c08.r
AI479358 tm27e07.x
AI324467 mi82b01.x
AI385490 mj81e03.y
AK008959 Mus muscu
AW86892 MR1-SN006
AK008886 Mus muscu
AI322423 mi82b01.y
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## ALIGNMENTS

FEATURES SOUTCE		AUTHORS TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM	RESULT 1 BG938320 LOCUS DEFINITION ACCESSION
COLIA=NO.  1472 1472 /organism="Bos taurus" /db_xref="taxon:9913" /clone_llb="Bovine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)" /ceil_type="Epithelial"	Tel: 780 492 0169 Fax: 780 492 0169 Email: Smoore@afns.ualberta.ca The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin) mrna) in main database at high score of 928.0 and E-value of 0.0 PCR PRimers FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 472	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G. cDNA's from bovine abomasum tissue Unpublished (2001) Contact: Dr. Stephen Moore Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada	EST.  COW.  Bos taurus  Bos taurus  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  Bovidae; Bovinae; Bos.	BC

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                                                                                                 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST project 1999
Unpublished (1999)
                                                      Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Marra, M., Hillier, L., Kucaba, T., Martin, J.,
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                                             TTTTGCCTCCAAATACTCAGTACCCATATTTGACAACATGATGAACAGGCACCTGGTGGC
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gtactggcaattcactgtggacagtgtcaccatcagcggtgtggttgttgcatgtgaagg
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Location/Qualifiers
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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: p7'73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
was primed with a Not I - oligo(dT) primer [5'
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Pred. No. 5.2e-91;
0; Mismatches 170;
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                                                          actacacaggatctcttcactgggttccagtcactgtgcagtactggcaattcactg 784
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Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Cetartiodactyla; Ruminantla; Pecora; Bovoldea
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Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA
mrna)in main database at high score of
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/sex="Two males and one female mixed"
/tlssue_type="castrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                 /dev_stage="Young adult"
/lab_host="XL1-BlueMRF/-strain"
/note="Organ: Abomasum; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                         Site_
130
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                                                                                                                                                                                                                   Score 354.8; DE Pred. No. 3.5e-9
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RESULT 4
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AI326975
AI326975.1
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This clone was previously sequenced on the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mj81e03.x1 Soares mouse IMAGE:482524 3' similar
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
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          Dr. Minoru Ko (Wayne State University)
                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
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AUTHORS
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Best Local Similarity 71.4
Matches 474; Conservative
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                                                                                                                                                                                                                                                                        CTCCAGTGGCTTC----AAGCAGGGCTCCCACATGTGGATCCTTGGGGATGTTTTCAT
                                                                                                                                                                                                                                                                                                                TGACCAGTTTGACATCGACTGCTGGAGGCTGGACATCATGCCCCACCGTTGTCTTTGAGAT
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                                                                                          sequence.
BG937723
BG937723.1
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                         BG937723
1Abo05D06 Bovine
        1 (bases 1 to 399)
Moore, S.S., Hansen,
                                                            Bos taurus
                                                                                 EST.
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 Hansen, C., Li, C bovine abomasum
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Pred. No. 4.8e-85;
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Contact: Dr. Stephen Moore
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   sequence.
AK004109
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The sequence best matches gb:BPU19786 (
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
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ays embryo whole body cDNA, RIKEN full-length
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  prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGGCCGCAACTCGAGTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA wen
                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                 Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409, 685-690 (2001)
5 (bases 1 to 1347)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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//db_xref="GI:12835164"
//db_xref="GI:12835164"
//tanslation="MKMINVLGLVALSECLVKIPLMKIKSMRENLRESQVLKDYLEKY
PRSRAHYLLEQRRNPAVTYEPMRNYLDLVYIGIISIGTPPQEERVVLDTGSSYLWVPS
IYCSSPACAHHKAFNPLRSSTFLVSGRPVNVAYGSGEMSGFLAYDTVRIGDLTVVAQA
FGLSLEEPGIFMEYAVEDGILGLGYPNLGLQGITPVFNNLMLQGLIPQNLFAFYLSSK
DEKGSMLMLGGVDFYYHGELHWYPVSKPSYMQLAVDSISMGEVIACDGGCQGIMDT
GTSLLTGPRSSIVNIQNLIGAKASGDGEYFLKCDTINTLPDIVFTIGSVTYPVPASAY
IRKDRSHNCRNNFEEGMDDPSDPEMWVLGDVFLRLYFTVFDRANNRIGLAPAA"
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/db_xref="MGD:MGI:1900662"
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                                                                                                                                                                                        Bovidae: Bovinae: Bos.

1 (bases 1 to 383)

Moore, S. S., Hansen, C., Li, C., CDNA's from bovine abomasum t CDNA's from bovine abomasum t Unpublished (2001)

Contact: Dr. Stephen Moore
. Beef Genomics Laboratory
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BG938086.1
EST.
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1AbollA08
                                                 Seq primer: T3 primer
High quality sequence
                                                                                                      Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786
mRNA, complete cds) in main database a
E-value of 0.0
                                                                                                                                                Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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                                                                                                                                                                                                                                                                                                                                             sequence.
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/organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 479 bp mRNA linear EST 11-t mil4c08.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:463502 5' similar to SW:CHYM_BOVIN P00794 PROCHYMOSIN PRECURSORS ;, mRNA sequence.
                                                     Contact: Marra M/Mouse EST Project
Washbr-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dul
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                         Unpublished (1996)
                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 479)
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38; Conservative
                                                                                                                                                                                                                                                                                                                                                                       house mouse
mouseest@watson.wustl
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I; Site_2: Xho I"
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
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RESULT 9
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                                   AI479358 505 bp mRNA linear EST 14-tm27e07.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157828 3' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
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Possible reversed clone: similarity on wrong strand
                   PRECURSOR ;, mRNA sequence.
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//db_xref="taxon:10090"
//clone_IMAGE:463502"
//clone_Lib="Soares mouse p3NMF19.5"
//dev_stage="19.5 dpc total fetus"
//lab_host="DB10B (ampicillin resistant)"
//lab_host="DB10B (ampicillin resistant)
//lab_host="Ty773D (pharmacla) with a modified
polylinker; Site_1: Not I; Site_2: Ecc RI; 1st strand cDNA
was primed with a Not I of Site_1: Not I of Site Selected, ligated to Eco RI
adapters (Pharmacla), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacla). Library went through, one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

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Pred. No. 1e-63;
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Local Similarity 77.
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                                                                                                   cagaaatggatcttgggagatgtgttcattcgtgagtactacagcgtctttgacagggcc 1140
                                                                                                                                                                                                 gcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaaccattcc 1080
                                                                                                                                                                                                                                                                                                 agctacatgcctacagttgtctttgagatcaacggcaagatgtacccactgaccccctcc 1020
                                                                                                                                                                                                                                                                                                                                                                                               caagctattggagccacacagaaccagtacggtgagtttgacatagattgcgacaacctt 960
                                                                                                                                                                                                                                                                                                                                                                        CAGGCCATTGGAGCCACTGCGGGCCAGTACAATGAGTTTGACATCGACTGCGGGCGCCTG
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                                                                                                                                                                    GCCTATACCAGCCAGGACCAGGGCTTTTGCACCAGTGGTTTCCAGGGTGACTATAGTTCC
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Location/Qualifiers
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/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soarses and M. Fatima Bonaldo. "
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/db_xref="taxon:9606"
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77.1%;
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RESULT 10
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426
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nes 343; Conserv
                             ggttgttgcatgtgaaggtggatgtcaagctatcttggataccggtacgtccaagctggt 869
                                                                        tccagtcactgtgcagcagtactggcaattcactgtggacagtgtcaccatcagcggtgt 809
                                                                                                                                                     GAGCATGCTCACACTGGGGGCCATCGATCAGTCATACTTCATAGGCTCACTGCACTGGGT
AGTGGTGGCTTGTCAAGGTGGCTGCCCTGCCGTTCTGGACACAGGCAATGCCCTGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project Washbrigton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lo Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rdx: 314 200 2000
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 546)
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                 normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:473065"
/clone_lib="Soares mouse p3NMF19.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            Minoru Ko (Wayne State University)." 140 c 140 g 132 t
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                                                                                                                                                                                                                                Score 246; DB 9;
Pred. No. 4.1e-59;
0; Mismatches 135
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RESULT 1
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VERSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caccagtggattccagagtgagaaccattcccagaaatggatcttgggagatgtgttcat 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI385490 517 bp mRNA linear EST 27-mj81e03.y1 Soares mouse p3NNF19.5 Mus musculus cDNA clone IMAGE:482524 5' similar to TR:Q28950 Q28950 PREPROCHYMOSIN PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                 MGI:293268
This read is a RESEQUENCE of a previously
This read has been verified (found to hit
                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                                                                                                                                                                                                                                                            correct orientation)
                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                             Possible reversed
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                                                                                                                                                                                                                            primer: -40RP from Gibco
                                                                                                                                                                                                           quality sequence stop:
/db_xref="taxxn:10090"
/db_xref="taxxn:10090"
/clone="IMAGE:482524"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: p777T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st str was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                  organism="Mus musculus
                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                               wrong strand
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     1st strand
[5'
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                                                             AUTHORS
TITLE
JOURNAL
MEDLINE
                     AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gatctacctcggaaccccgcctcaagagttcaccgttctctttgatactggttcctctga 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgagatcaccogcattcctctacaaaaggtaagtctctccgtaaggcgctgaaggaaca 137
                                                                                                                                                                                                                                                                                                                                                                                                               tcaacagacagtaggacttagcacccaagaacc 530
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTAGAATGGAGGGCTTCCTGGCCTACGACACTGTCACAGTCTCTGATATTGTAGTGTN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaacattgtggacat 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCTGGGTACCCTCTGTCTACTGCAACAGCAAAGTGTGCCGAAACCACCACCGTTTTGA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCTACATTGGGACACCACCGCAGGAGTTCACCGTGGTGTTTGACACAGGCTCCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCGGGGTGGTCGCCAGTGAGCCTCTGATCAACTATCTAGATAGTGAGTACTTTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cttcggtgaagttgctagcgtgccacttaccaactaccttgatagtcaatactttgggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGACTGCTGGAGGACTTTCTGAGCAGACAGCAGTACGAGTTCAGTGAGAAGAACTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321;
                                                                                                                                                                                       HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
    Carninci, P., Sh
Itoh, M., Konno,
                                                                                                                                                                                                                                                                            AK008959 1385 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library clone:2210416016:homolog to GASTRICSIN PRECURSOR (EC
                                                         99279253
                                                                                                                                                                             clone:2210416016.
                                                                                                                                                                                                                     AK008959.1 GI:12843460
HTC; CAP trapper.
                                                                                                                                                                                                                                                     AK008959
                                                                             Meth.
                                                                                        High-efficiency
                                                                                                       Carninci, P. and Hayashizaki, Y.
                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                               AK008959
                                               10349636
                                 (sites)
                                                                                                                       (sites)
                                                                                                                                                                 musculus
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                                                                       Enzymol.
                                                                                                                                                                                                                                                                 3) (PEPSINOGEN C),
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10,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%;
                                                                         full-length cDNA cloning
103, 19-44 (1999)
                                                                                                                                 Chordata;
Rodentia;
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Pred. No. 4.2e-58;
D; Mismatches 132
                                                                                                                                                                                                                                                                 full insert sequence.
                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGGARCCAAAGACTCTTTTTTTTTTTTTTTTTVN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction Rot = 25.0. Second strand cDNA was prepared with the primer adapter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
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                                                                                                                                                                                                                                                                                                                                                                                                                with XhoI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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e RIKEN Genome
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                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="MGD:MGI:1895643"
/db_xref="taxon:10090"
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                                                                                                    /sex="male"
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                                  TACCTTGGCAGCCAGCAGGGGTCTAACGGCGGGCAGATTGTGTTCGGTGGCGTGGACGAG
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GIVDTGTSLLVMPAQYLNELLQTIGAQEGEYGQYFVSCDSVSSLPTLTFVLNCVQFPL
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Pred. No. 4.2e-56;
0; Mismatches 483
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                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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MR1-SN0064-150500-004-a03
                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-SN0064-150500-004-a03&t3=2000-05-15&t4=1)
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Fax: +55-11-2707001
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AKO08886

Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210410L06:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
                                                  Mus musculus
                                                                                                 Mus musculus (strain:C57BL/6J) adult male stomach cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                               clone: 2210410L06.
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HTC; CAP trapper.
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  ; Metazoa; Chordata;
Eutheria; Rodentia;
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/dev_stage="Adult"
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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotrani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, F., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagama, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                    URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
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                           ggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaagaaccac
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1895666"
/db_xref="taxon:10090"
/clone="2210410L06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB25952.1"
/db_xref="G1:12843350"
/db_xref="G1:12843350"
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/db_xref="G1:12843350"
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/translation="MKMMVVALLCLPLLEAALIRVPPKKMKSIRETMKEQGVLKDFLKVV
KYDEQKYLEFGKFGDYSVLYEPMAYMDASYYGEISIGTPFQNETLRVQSIQVPN
QEFGLSENEPGTNFVYAQFDGIMGLAYPGLSSGGATTALQGMLEGALSQPLFGVYLG
QEFGLSENEPGTNFVYAQFDGIMGLAYPGLSSGGATTALQGMLEGALSQPLFGVYLG
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SQQCGIVDTGTSLLYMPAQYLNELLQTIGAQEGEYGQYFVSCDSVSSLPTLYFVLNGVQFPL
SPSSYIIQEEGSCMVGLESLSLNAESGQPLMILGDVFLRSYYASSTMAITGMALPLLS
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/clone_lib="RIKEN full-length
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mi82b01.y1 Soares mouse
IMAGE:473065 5' similar
                                                                                                                                                                                                     Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                        This read is a RESEQUENCE of This read has been verified
                                                                                                                                                                                                                                                                                                                                    Theising, B., Wylie, T., Lennon, G., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                           vector to vector
                                                                          Putative full length read
                                                                                           correct orientation)
                                                                                                                                          MGI:283809
                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
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                                            primer: -40RP from Gibco
                          quality sequence stop: 395
         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 bp mRNA linear p3NMF19.5 Mus musculus cDNA to TR:Q28075 Q28075 CHYMOSIN
                                                             655
                                                                                                          (found to hit
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                                                                                                          sequenced mouse its original se
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Matches 297;
             941 acatagattgcgacaaccttagctacatgcctacagttgtcttttgagatcaacg 994
                                                                                                                                                                  641 tagtagctcaagacttgttctcggtttacatggacaggaatggccaggagagcatgctca 700
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                                                    301 GAGACATCCTCAATATTCAGCAAGTCATTGGAGCTGTGCAAGGCCATAATGACCAGTTTG
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                                                                    gcgacattctcaacattcagcaagctattggagccacacagaacccagtacggtgagtttg
                                                                                                           GTCAAGGTGGCTGCCCTGCCGTTCTGGACACAGGCACTGCCCTGTTGACGGGGCCTGGTA
                                                                                                                              gtgaaggtggatgtcaagctatcttggataccggtacgtccaagctggtcggacctagca 880
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Pred. No. 1.1e-53;
0; Mismatches 117; Indels
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BASE COUNT ORIGIN

Search completed: July 31, 2002, 15:44:34 Job time: 13695 sec

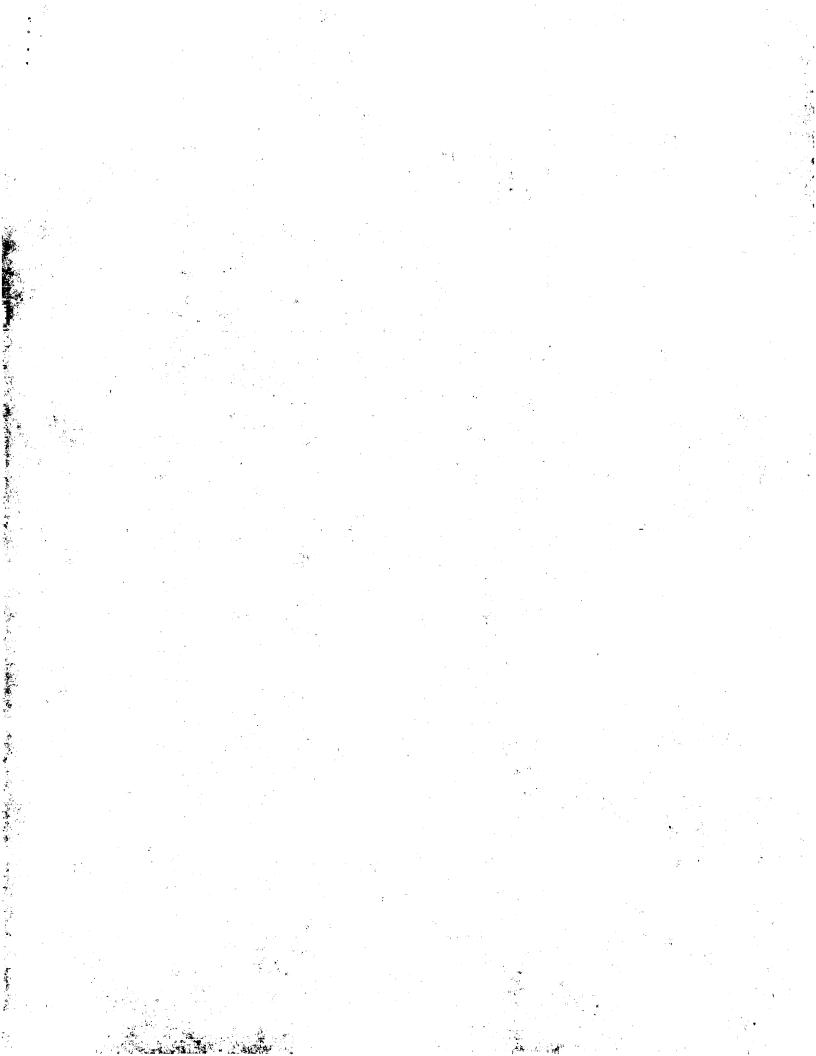
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                Score
A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

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15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Com
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AAR05080
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                 Prochymosin. AAP
Sequence encoded b
Pre-prorennin-A pr
Sequence of calf p
                                                                                                        Bovine chymosin po
BamHI/Sall insert
Oleosin-spacer-Met
Sequence of a poly
Sequence encoded b
Sequence of rennin
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## ALIGNMENTS

AAU00536 RESULT

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AAU00536 standard; Protein;

390

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AAU00536;

14-MAY-2001 (first entry)

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Chymosin; transcription regulator; terminator sequence; soybean; corn; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba.
                                                                                                                                  Key
Peptide
                           23-AUG-2000; 2000WO-CA00975
                                                                                                                                                                Bos sp.
                                                                                                                                                                                                                                            Bovine chymosin polypeptide sequence.
         23-AUG-1999;
                                                                 WO200114571-A1
                                                                                              Protein
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         99US-0378696
                                                                                  /note= "Pro sequence"
68..390
/note= "Mature chvm^o"
                                                                                                                                  Location/Qualifiers 1..26
                                                                                                               /note= "Signal peptide" 27..67
                                                                                   "Mature chymosin"
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Sequence encoded

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RESULT
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XX AAP9
XX IS-J
DT 15-J
XX BamF
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XX Kluy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a bovine chymosin polypeptide. Chymosin can be produced in a plant seed through introduction of a chimeric nucleic acid molecule, comprising a nucleic acid sequence encoding a chymosin polypeptide operatively linked to transcription regulator and terminator sequences, into a plant cell. The sequences are useful for producing plant seeds, in particular seeds of soybean, rape seed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, Arabidopsis thaliana, potato, flax/linseed, safflower, oil palm, groundnut, Brazil nut, coconut, castor, coriander, squash, jojoba and rice.
           Kluyveromyces
                               Kluyveromyces;
                                                  BamHI/Sall insert of Kluyveromyces plasmid pAB309
                                                                        15-JUN-1990
                                                                                                               AAP94376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing chymosin in seeds of plants such as rice, flax, rape seed, by transforming plant cell with a nucleic acid encoding chymosin operably linked to transcription regulator and terminator sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Mismatches 0;
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                     29-NOV-1999
                                                           AAY33830
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366; Conser
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                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
                    (first entry)
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amino acid sequence.

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Kluyveromyces host cells for producing polypeptide(s) - used for highly efficient prodn. of eg chymosin tissue plasminogen activator or human serum albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KONN ) GIST-BROCADES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kluyveromyces expression systems provide highly processing of a wide variety of proteins. uences identical to those published in EP301669.
                                                                                                                                                      1989-033565/05.
DB; AAN91188.
                                                                                                                                                                                                                            svtisgvvvaceggcqaildtgtsklvgpssdilniqqaigatqnqygefdidcdnlsym
                                                                                                                                                                                                                                            SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                                                                                                                                                                  pvfdnmnrhlvaqdlfsvymdrngqesmltlgaidpsyytgslhwvpvtvqqywqftvd
                                                                                                                                                                                                                                                                                                                  PVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVD
                                                                                                                                                                                                                                                                                                                                                                       ygtgsmggilgydtvtvsnivdigqtvglstqepgdvftyaefdgilgmaypslaseysi
                                                                                                                                                                                                                                                                                                                                                                                        YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                         FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 2.2e-174;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             incorporated into plasmids pAB309 with 18 resistance marker fused to a ADH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rietveld
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C B.napus plants.

C B.napus plants.

C B.napus plants.

C B.napus plants.

C oil-body targeting sequence, a transcription regulation sequence and the coll-body targeting sequence, a transcription regulation sequence and the protein of interest can be used to produce antibodies, proteases, proteases inhibitors, seed storage proteins, thrombin inhibitors, proteases inhibitors, seed storage composed the proteins, thrombin inhibitors, proteins, interleukins, chymosin, cystatin, cxylanase, carp growth hormone, zein or a collagenase.

C xylanase, carp growth hormone, zein or a collagenase.

C xylanase, carp growth protein or used in cassociation with the oil body fraction.

C allows production of commercially important proteins on a superior scale to production by conventional systems. The expressed heterologous protein can be easily separated from host cell components

C protein can be easily separated from host cell components

C due to the use of the oil body as a carrier protein.
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                                                                                                Query Match
Best Local S
Matches 368
                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of a HindIII fragment containing the oleosin-spacer-Met-prochymosin sequence. This HindIII fragment was joined to a nopaline synthase terminator and cloned into binary vector pCGN1559. The resulting plasmid was called pSBSOTPTNT and introduced into A.tumefaciens. The resulting bacterial strain was used to transform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oil-body; lipid bo
fusion protein; he
plasmid; oil-body
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression of a heterologous useful for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1991;
16-NOV-1993;
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                                     PLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTF
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Similarity
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91US-0659835.
93US-0142418.
94US-0366783.
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182..483
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176..181
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119..175
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Pred. No. 8.3e
1; Mismatches
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3.3e-174;
hes 6;
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                                  Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase with B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
Sequence
                                                                                                                                                                   Claim
                                                                                                                                                                                                          Recombinant DNA coding for 
expressed in transformed
                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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Query Match Best Local Similarity

93.1%; 98.4%;

Score Pred.

1922; DB 5; No. 1.8e-173;

Length 381

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RESULT AAP4 OO718 ID AAP4
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rue inventors claim the prochymosin gene comprising a nucleotide sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinan plasmids harboured by Escherichia coli strains deposited as FENA 262, -263 and -264. Any portion of the nucleotide sequence as described in AAN40055 can be used. Also claimed is a vector deriftrom plasmid pBR322. Typically plasmid pCR501 is obtd. from pOCT
                                                                                                                                                                                                                               Expression plasmid comprising prochymosin gene useful for transforming Escherichia coli for pr
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                  DNA segment contg. GAL1 direction of expression
                                                                               N-PSDB;
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Best Loc
Matches
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                                                                                                                Lactic acid bacteria; proteinase; pSK112; c
                                                                                                                                                                                                   AAP94144 standard;
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                         (NEZU-) NEDERL INS ZUIVELON
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nnlvglakai 381
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       Vos
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                                                                                                                                                                                                  protein;
                                                                                                                  a; cheese;
chymosin;
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Pred. No. 3.5e-173;
2; Mismatches 4; Indels
                                                                                                                 Streptococcus cremoris prochymosin.
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Best Local S
Matches 364
                                             Key
Region
                                                                           Cow.
         Region
                            Region
                                                                                           Milk-clotting; cheese making;
                                                                                                               Sequence
                                                                                                                                  03 - AUG
                                                                                                                                                     AAP30446;
                                                                                                                                                                        AAP30446 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA encoding prochymosin can be cloned into a plasmid (esp. from S. cremoris SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome shortages of prochymosin due to a shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAP94145 and AAP94146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-030097/04.
N-PSDB; AAN91157.
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                                                                                                                                                                                                                                         LAKAI 390
                                                                                                                                                                                                                                                                               VVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVG
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364; Conservative
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59..381
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                                                                                                               preprochymosin cDNA
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                                    preprochymosin
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Pred. No. 4.1e
0; Mismatches
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1.1e-173;
nes 1;
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Best Local Similarity
Matches 364; Conserv
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                Pre-prorennin-A
                                                                AAP20038
                                                                                                                                                                                                                                                                                                                                                                                              prochymosin and chy prochymosin primer.
                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a method for the prodn. of calf stomach chymosin for cheese making. Genes and polypeptides for preprochymosin, prochymosin and chymosin are claimed, as are vector systems and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodn. or calf stomach chymosin for cheese cultivation of micro-organisms transformed
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                                                                                                                                       SIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASE
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prorennin;
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Pred. No. 4.3e-173;
3; Mismatches 3;
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enzyme;
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chymosin;
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Best Local :
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16-JAN-1981;
                                                                                                                                                                                                                                                                                Sequence
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371
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                                                                                                                                                                                                     NNLVGLAKAI 390
                              SYMPTYVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA 380
nnlvglakai
                                                                                                                                                                                                                                              Similarity
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81US-0225717.
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380
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98.1%;
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Pred. No. 1e-172;
2; Mismatches 5; Indels
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05-OCT-1990

(first entry)

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RESULT 1
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Best Local Similarity
Matches 362; Conserv
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plasmid
Sequence encoded by prorennin cDNA in
               14-JUN-1992
                                           AAP30603 standard;
                                                                                                                                                                                                                                                                                                                     Sequence
                             AAP30603;
                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                    Complex plasmid and microbe -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP02109984-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of calf
                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                       (VEPP ) VEPPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro-rennin;
                                                                              361
                                                                                            386
                                                                                                          301
                                                                                                                                                                                                           146
                                                                                                                                      241
                                                                                                                                                                 181
                                                                                                                                                                                              121
                                                        11
                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                     <u>_</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             taurus
                                                                                                       AEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQYFG 85
                                                                              lakti 365
                                                                                            LAKAI 390
                                                                                                                                                                                                    TGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPV
                                                                                                                                                                                                                                KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                                                                                                                                                                                                                                                                                                                                          1990-168358/22
                                                                                                                                                                                           tgsmqgilgydtvtvsnivdiqqtvglstqepgdvftyaefdgilgmaypslaseysipv
                                                                                                                                                                                                                        kiylgtppqeftvlfdtgssdfwvpsiycksnacknhqrfdprksstfqnlgkplsihyg
                                                                                                                                                                                                                                                                                                                                  pBR322.
                                                                                                                                                                                                                                                                                                                                                                                   AAQ04683
                                                                                                                                                                                                                                                                                                                                        product may
                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                      32; 13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds
                                                                                                                                                                                                                                                                                  Conservative
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      88JP-0302176
                                                                                                                                                                                                                                                                                                                                                                                                                                   88JP-0302176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pro-rennin
                                          Protein;
                                                                                                                                                                                                                                                                                                                                        be
                                                                                                                                                                                                                                                                                       92.5%;
                                                                                                                                                                                                                                                                                                                                                      Japanese.
                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                Score 1910; DB 11;
Pred. No. 2.3e-172;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                   contains calf pro-rennin
                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                         E.coli
pcR 10001
                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                       system
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                              265
                                                                                                                                                                                                          205
                                                                                                                                                                                                                        120
                                                                                                                       385
                                                                                                                                                 325
                                                                                                                                                                                            180
                                                                                                                                                                240
                                                                                                                                                                                                                                                                                0
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RESULT 1
AAP30013
ID AAP3
XX
AC AAP3
XX

AAP30013 standard;

peptide;

379

A

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AAP30013;

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В
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                                                                     Вb
                                                                                  Qy
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                                                                                                                       Ωy
                                                                                                                                         B
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                                                                                                                                                                               밁
                                                                                                                                                                                              Qy
                                                                                                                                                                                                                В
                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                             The inventors claim recombinant plasmids contg. the cDNA of calf prorennin. Specified plasmids are pCR 10001 and pCR2001 (contg. the whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coll CR1 (ATCC 391710) contg. plasmid pCR2001.
                                                                                                                                                                                                                                                                                                                                                                    Example; Page 20-23; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                     microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                Plasmid contg. calf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-1981;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Beppu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BEPP/) BEPPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rennin; renin;
                386
                                 301
                                                                                       266
                                                                                                        181
                                                                                                                                          121
361
                                                                     241
                                                                                                                         206
                                                                                                                                                             146
                                                                                                                                                                           61 kiylgtppqeftvlfdtgssdfwvpsiycksnacknhqrfdprksstfqnlgkplsihyg
                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                  Local Similarity 98.9
mes 361; Conservative
                                                                                                                                                                                                               1983-22976K/10.
DB; AAN30063.
                LAKAI 390
                               TISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT 325
                                                                                                     KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                   tisgvvvaceggcqaildtgtsklvgpssdilniqeaigatqnqydefdidcdnlsympt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                           Uozumi T,
365
                                                                                                                                                                                                                                                                                                365
                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81JP-0131631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82EP-0107601
                                                                                                                                                                                                                                                           92.48;
                                                                                                                                                                                                                                                                                                                                                                                               pro:rennin DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease
                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                  Score 1907; DB 4;
Pred. No. 4.5e-172;
1; Mismatches 3;

    and transformed

                                                                                                                                                                                                                                                                  Length 365;
                                                                                                                                                                                                                                                   Indels
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RESULT 1
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Best Local S
Matches 362
                                                                                                                                                                                                               from calves, and plasmids contg. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-15061). The microorganisms transformed by the plasmid are also claimed.
                                                                                                                                                                                                                                                                                                                                                                               Protolytic enzyme;
                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                               13-APR-1983;
01-JUL-1982;
                                                                                                                                                                                                                                                                                                                                30-JUN-1983;
                                                                                                                                                                                                                                                                                                                                           03-NOV-1983
                                                                                                                                                                                                                                                                                                   (GENE-) GENEX
                                381
                                                                                        190
                                                                                                             130
                      370
                                                       321
                                                                             261
                                                                                                  201
                                                                                                                        141
                                                                  250
                                                                                                                                                                              Local Sin
hes 362;
                                                                                                                                             81
                                                                                                                                                        10
      13
                                                                                                                                                                                                                                                              lated chymosin or rennin and prochymosin genich replicate in prokaryotic organisms, esp. organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                taurus
                                                                 NNLVGLAKAI
                                                                                                           nnlvglakai
                                                                                                                                                                  AVTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLD 80
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                           encoded
                                                                                                                                                                                                                                                    Page 33-36; 43pp; French.
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                     CORP
                                                                                                                                                                                                                                                                                                               83US-0484539.
82US-0394433.
                                                                                                                                                                                                                                                                                                                                83BE-0017731.
                                                                                                                                                                                                                                                                                                                                                                                zymogen;
                                                                                                                                                                                   92.2%;
                                                                                                                                                                                                                                                                                                                                                                                rennin; chymosin;
                                                                                                                                                                              Score 1903; D
Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                              DB 4;
l.le-171;
les 5;
                                                                                                                                                                                                                                                                                                                                                                                 cheese
                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                        Length 379;
                                                                                                                                                                                                                                                                                                                                                                                making;
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Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                                                Sequence
allelic 1
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                     Maat
                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                      AAP30086 standard; Protein;
                                                                                                                                                                                                                                                               (UNIL )
                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                       192
                                                             132
                                                                       141
                                                 201
                                                                                              81
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DNA molecules comprising genes for preprochymosin - utransform microorganisms to give strain producing the prepro-enzyme and its allelic and maturation forms
                                                                                                                                                                                                                                                                                                                                                                                                                                               clotting component of rennet AAN30049 corresp. to mRNA is preruminant calf (abomasum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                preprochymosin is an intermediate (via prochymosin and pseudochymosin) for the enzyme chymosin, which is the essential pseudochymosin of the enzyme chymosin, which is the essential clotting component of rennet and is used in cheese manufacture. AAN30049 corresp. to mRNA isolated from the fourth stomach of a
                321
                                                                                                                                                                                                                                                                                 SYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNILEVER
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forms (B)
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82EP-0201272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by cDNA sequence corresponds of bovine preprochymosin
                                                                                                                                                                                                                                                                                                                                                            92.2%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ledeboer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frisian
                                                                                                                                                                                                                                                                                                                                                            Score 1903;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑM,
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                             ; DB 4;
1.1e-171;
hes 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                         Length 381;
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312

symptvvfeingkmypltpsaytsqdqgfctsafqsenhsqkwilgdvfireyysvfdra 371

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RESULT 14
AAA20730
ID AAA207
XX AAA207
XX AAA207
XX AAA207
XX AAA207
XX Rennet
KW Rennet
KW Clotti
XX Bos ta
XX FT Protei
FT Peptid
FT Cleava
FT Cleava
FT Cleava
FT Misc-(
FT M
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                                 The prorennin (prochymosin) sequence was deduced from the DNA sequence obtd. by screening a cDNA library with rennin specific probes derived from the published amino acid sequence of rennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see 232291,2). The deduced protein sequence was the same as the published sequence after cleavage of the signal peptide, except for an amino acid change at residue 218, which may be an artefact of protein sequencing in the original sequence. The cleavage product of protein sequencing in the original sequence. The cleavage product of protein B. The cleaved synthesised in two active forms rennin A, and rennin B. The cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1988;
11-MAY-1984;
12-DEC-1986;
31-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-049149/06.
N-PSDB; AAQ20949.
                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                             bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BERL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prochymosin (prorennin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR20730
                                                                                                                                                                                                                                                                                                                                        Isolating heterologous po-
bodies - by lysing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rennet;
                                                                                                                                                                                                                                                                                                                   insoluble polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NNLVGLAKAI 390
||||||||||
2 nnlvglakai 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zymogen; au
g activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BERLEX LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                   protein undergoes activation
                                                                                                                                                                                                                                                                     Fig 6; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88US-0263927
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306
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59..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= signal_peptide
43..44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- preprorennin
/note- "also known as preprochymosin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autocatalytic activation; pseudorennin; milk;
y; renin A, renein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "autocatalytic cleavage
                                                                                                                                                                                                                                                                                                                                        polypeptide from bacterial inclusion
ls, extn. with nonionic detergent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "amino acid determining
of rennin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "autocatalytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                     in the acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence'
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             plasminogen
                    Kluyveromyces host cells for producing polypeptide(s) - used for highly efficient prodn. of eg chymosin tissue
                                                                                                                           01-JAN-1989
                                                                                                                                                                                                      AAP94370
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                                           N-PSDB;
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                                                                               (KONN)
                                                                                              28-JUL-1987;
                                                                                                             28-JUL-1988;
                                                                                                                                                         Kluyveromyces;
                                                                                                                                                                       Sequence encoded by
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                                                                                                                                                                                                                     AAP94370 standard;
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DB; AAN91185.
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             activator
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                                                                                                                                                         pDM100PC; chymosin; tissue plasminogen activator.
                                                                                              87US-0078539
                                                                                                             88EP-0201632
                                                                                                                                                                                                                                                                        390
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                                                                van
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                                                                                                                                                                       BamHI insert from pDM100PC
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             or
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             human serum
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Disclosure; ; 56pp; English

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Local Similarity 95.7%;
nes 355; Conservative
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|pnnlvglakai 450
                                        FTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDN 319
                                                                                                                         LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
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Pred. No. 8.2e-169;
5; Mismatches 11;
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Search completed: July 31, 2002, 09:20:52 Job time: 1554 sec

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Copyright (c) 1993 - 2000 Comp
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pepsinogen A (EC 3.4.2)
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35.3	36.0	36.2	37.5	38.0	38.4	38.6	39.7	40.0	40.9	41.6	41.8	42.0	42.1	42.4	43.2
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cathepsin D (EC 3.	pregnancy-specific	pregnancy-associat	cathepsin D (EC 3.	pregnancy-associat	cathepsin E (EC 3.	pepsin C (EC 3.4.2	aspartic proteinas	pepsinogen C - com	gastricsin (EC 3.4	gastricsin (EC 3.4	gastricsin (EC 3.4	gastricsin (EC 3.4			

## ALIGNMENTS

## N;Alternate names: preprochymosin; preprorennin; rennin B N;Contains: chymosin; prochymosin C;Species: Bos primigenius taurus (cattle) C;Date: 24-Apr-1984 #sequence\_revision 09-Sep-1994 #text\_change 18-Jun-1999 C;Accession: A25631; A93419; A44608; A92259; A44620; A91935; A91495; D22434; A00985 R;Hidaka, M.; Sasaki, K.; Uozumi, T.; Beppu, T. Gene 43, 197-203, 1986 A;Title: Cloning and structural analysis of the calf prochymosin gene. A;Reference number: A25631; MUID:86301873 A;Accession: A25631 A;Accession. A;Accession. A;Accession. A;Accession. A;Accession. A;Residues: 1-229,'N',231-381 <HAR> A;Residues: 1-229,'N',231-381 <HAR> A;Cross-references: GB:J00003; NID:g162859; PIDN:AAA30448.1; PID:g162860 A; Molecule type: DNA A; Residues: 1-16, 'T', 18-381 <HID> R; Harris, T.J.R.; Lowe, P.A.; Lyons, A.; Thomas, P.G.; Nucleic Acids Res. 10, 2177-2187, 1982 A; Title: Molecular cloning and nucleotide sequence of C. A; Reference number: A93419; MUID:82221400 A; Molecule type: protein A; Residues: 17-173,'T',175-217,'D',219-251,'Y',253-381 <FO2> R; Cchang, W.J.; Takahashi, K. J. Biochem. 76, 467-474, 1974 A; Molecule type: protein 4; Residues: 59-217, Dr., 219-381 <FOL> R; Foltmann, B.; Pedersen, V.B.; Jacobsen, H.; Kauffman, D.; Wybrandt, Proc. Natl. Acad. Sci. U.S.A. 74, 2321-2324, 1977 A; Title: The complete amino acid sequence of prochymosin. A; Reference number: A44620; MUID: 77234648 A; Accession: A44620 J. Biol. Chem. 254, 8447-8456, 1979 A;Title: The primary structure of calf chymosin. A;Reference number: A92259; MUID:79239460 A;Contents: chymosin B; disulfide bonds A;Accession: A92259 A;Molecule type: mRNA A;Residues: 7-14,'X',16-42,'L',44-87,'N',89-301,'D',303-324,'I',326-334,'G',336-342,'A;Cross-references: GB:J00004 A;Cross-references: GB:J00004 R;Nishimori, K.; Kawaguchi, Y.; Hidaka, M.; Uozumi, T.; Beppu, J. Biochem. 91, 1085-1088, 1982 A;Title: Nucleotide sequence of calf prorennin cDNA cloned in A;Reference number: A44608; MUID:82189915 R;Foltmann, B.; Pedersen, V.B.; Kauffman, D.; Wybrandt, J. Biol. Chem. 254, 8447-8456, 1979 chymosin (EC 3.4.23.4) precursor -A; Note: authors translated A; Accession: A93419 A; Contents: prochymosin B A; Accession: A44608 the codon TTG bovine for sequence of cDNA coding for calf preprochym residue 43 Eaton, M.A.W.; Millican, S S Phe, Escherichia ACC <u>و</u> coli

A; Title: The structure and function of acid proteases. III. Isolation and characteriz

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A;Reference number: A91935; MUID:75060332
A;Contents: active site peptides
A;Accession: A91935
A;Accession: A91935
A;Molecule type: protein
A;Residues: 92-96;274-278,280 <CHA>
A;Residues: 92-96;274-278,280 <CHA>
A;Residues: D: Mao, J: Schumm, J.W.; Vovis, G.F.; Alford, B.L.; Taunton-Rigby, A.
Residues: 1-18, 182
Gene 19, 127-138, 182
A;Title: Molecular cloning and characterization of double-stranded cDNA coding for by A;Reference number: A91495; MUID:83054629
A;Contents: prochymosin A
A;Residues: 1-301, D', 303-381 <MOID
A;Residues: 1-301, D', 304-341, MUID:86059312
A;Rocession: D22434
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chymosin (EC 3.4.23.4) B precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammore
C;Date: 30-Sep-1991 #sequence_revision 30-
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#text_change 18-Jun-1999
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A;Cross-references: EMBL:X53037; NID:gl373; PIDN:CAA37209.:
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; gastric juice; hydrolase;
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-58/Domain: activation peptide #status predicted <APT>
F;59-381/Product: chymosin B #status predicted <MATY>
F;92,274/Active site: Asp #status predicted
F;105-110,265-269,308-341/Disulfide bonds: #status predict.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S10996
R;Pungercar, J.; Strukelj, B.; Gubensek, F.;
Nucleic Acids Res. 18, 4602, 1990
A;Title: Complete primary structure of lamb
A;Reference number: S10996; MUID:90356410
A;Accession: S10996
                                                                                                                                                                                                                                                               RESULT
JC7247
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A; Residues: 1-381 < PUN>
C; Superfamily: pepsin C; Keywords: gastric j
                              A; Experimental source: strain NW813
C; Comment: This protein, a zymogen of pepsins, volution of mammalian orders and families.
                                                                             A; Molecule type: mRNA
A; Residues: 1-381 <KAG>
A; Cross-references: DDB
                                                                                                                           A; Title: New world monkey pepsinogens A; Reference number: JC7245 A; Accession: JC7247
                                                                                                                                                                                                                   prochymosin - common marmoset
C; Species: Callithrix jacchus (common marmoset)
C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2
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                                                                                                                                                                                                                                                                                                                                                                                                          SYMPTYVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRA 380
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93.2%;
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Pred. No. 8.7e-137;
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Score

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Length

381;

81.4%;

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A;Molecule type: mRNA
A;Residues: 1-380 <FOL>
A;Cross-references: EMBL:U14406; NID:g540096; PIDN:AAB08492.1;
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase
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                                                                                                LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
                                                                                                                      DTQYFGKIYIGTPPQEFTVVFDTGSSELWVPSVYCKSDACQNHHRFNPSKSSTFQNLDKP
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Pred. No. 8.8e-119;
95; Mismatches 39;
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D; Mismatches 39;
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pepsinogen A - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 30-Jun-2001 #sequence_revision
C;Accession: JC7575
R;Ikuzawa, M.; Inokuchi, T.; Kobayashi,
J. Biochem. 129, 147-153, 2001
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R; Kageyama, T.

J. Biochem. 127, 761-770, 2000
A; Title: New world monkey pepsinogens A and C
A; Reference number: JC7245
A; Accession: JC7245
A; Molecule type: mRNA
A; Residues: 1-387 < KAG>
A; Cross-references: DDBJ: AB038384
A; Cross-references: DDBJ: AB038384
A; Experimental source: strain NW794
C; Comment: This protein, a zymogen of pepsins volution of mammalian orders and families.
C; Superfamily: pepsin
C; Keywords: gastric juice; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pepsinogen A - common marmoset
c:Species: Callithrix jacchus (common marmoset)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2
C:Accession: JC7245
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JC7245
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ver

30-Jun-2001 #text\_change

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A;Molecule type: mRNA
A;Residues: 1-385 <IRV>
A;Cross-references: DDBJ:AB045376
C;Comment: This protein is a zymo
C;Genetics:
                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-383 <HAX'>
A; Cross-references: GB:D00215; NID:g2760810; PIDN:BAA00153.1;
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; hydrolase; protein digestion
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                                                                                                                                                                                                     A;Title: Molecular cloning and the nucleotide A;Reference number: A41443; MUID:88227903 A;Accession: A41443
                                                                                                                                                                                                                                                                       pepsin (EC 3.4.23.-) precursor, embryonic - chicken C;Species: Gallus gallus (chicken) C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 C;Accession: A41443
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                      Q
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Best Loc
Matches
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                                                    Query Ma
Best Loc
Matches
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;Keywords: stomach;
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                         11
                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEPLQNYMDIEXFGTISIGTPPQSFTVIFDTGSSNLWVPSVYCSSPACTNHHMFNPQQSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLFG---LVVLAECGVVKVSLRKGESLRARLNRLGLLGDYLKKHHYNPATKYFPSLAQAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSEN----HSQKWILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAFPSLASSQATPVFDNMWNQGLIPQDLFSVYLSSQGQSGSFVLFGGVDTSYYTGNLNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFQATNTPVSIQYGTGSMSGFLGYDTVQVGNIQITNQIFGLSQSEPGSFLYYSPFDGILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSS 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLTAETYWQITVDSISIGGQVIACSGSCSAIVDTGTSLLAGPSTPIANIQYYIGANQDSN
                         AFLCFGQYFVAVTHAAE-ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFG 68
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213; Conser
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-AVLALSDGITRLPLERGKKLREILREKGLLHHFLQHHRYDIGTKFPHAFP
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55.9%;
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                                                       68;
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                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 3.7e-79
                                                                    1094.5;
No. 9.16
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                                                95;
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                                                                           TQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQD-QGFCTSGFQSENHSQKWI
                                                                                                                                                                    FDGILGLGYPSLAADGITPVFDNMVNESLLEQNLFSVYLSREPMGSMVVFGGIDESYFTG
                                                                                                                                                                                FDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTG
                                                                                                                                                                                                                           \tt NPSQSSTYKSTGQNLSIHYGTGDMEGTVGCDTVTVASLMDTNQLFGLSTSEPGQFFVYVK
                                                                                                                                                                                                                                          DVLTVVTEPLLNTLDMEYYGTISIGTPPQDFTVVFDTGSSNLWVPSVSCTSPACQSHQMF
                                                                                                                                                                                                                                                                                                  EVASV---PLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRF
              LGDVFIREYYSVFDRANNLVGLAKAI
                                                                                                             SLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGA
LGDVFIRVYYSIFDRANNRVGLAKAI
                                                     NQNTYGEYSVNCSHILAMPDVVFVIGGIQYPVPALAYTEQNGQGTCMSSFQNSS-ADLWI
    383
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In by 4 months of age.

C;Comment: Although two-step activation is observerd, activation is predominantly a C;Comment: Although two-step activation is observerd, activation is predominantly a C;Superfamily: pepsin c;Ckeywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein; protein d;F;1-15/Domain: signal sequence #status predicted <SIC>F;16-388/Product: pepsinogen A 2/3 #status experimental <APT>F;63-388/Product: pepsin A 2/3 #status experimental <ENZ>F;63-388/Product: pepsin A 2/3 #status experimental F;40-41/Cleavage site: Asp-Phe (pepsin) #status experimental F;40-61/Cleavage site: Leu-Ile (pepsin) #status experimental F;40-61/Cleavage site: Leu-Ile (pepsin) #status experimental F;40-27/Active site: Asp-Phe (pepsin) #status experimental F;40-27/Active site: New Holding Fillowship #status predicted F;107-112,268-272,311-344/Disulfide bonds: #status predicted F;107-112,268-272,311-344/Disulfide bonds: #status predicted C;Accession: S19684; SIDVON
R;Kageyama, T.; Tanabe, K.; Koiwai, O.
R;Kageyama, T.; Tanabe, K.; Koiwai, O.
Eur. J. Biochem. 202, 205-215, 1991
A;Title: Development-dependent expression
A;Title: Dayelopment S19681; MUID:92037645 pepsin A (EC 3.4.23.1) 2/3 precursor - Japanese macaque N;Alternate names: pepsinogen A isozyme 2/3 C;Species: Macaca fuscata (Japanese macaque) C;Date: 22-Nov-1993 #sequence\_revision 19-Oct-1995 #text\_change C;Accession: S19684; S16064 A;Cross-references: EMBL:x59755; NID:g38068; PIDN:CAA42427.1; PID:g38069 A;Note: parts of sequence, including amino ends of pepsinogen and activa C;Comment: It could not be determined if this sequence represents isozym A; Molecule type: mRNA A; Residues: 1-388 < KAG> A; Accession: S19684 of isozymogens of monkey 18-Jun-1999 activation intermed isozyme 2 or 3, whi pepsinogens and

В

137

144

YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203

YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT

196

FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143 IHKVPLVRKKSLRRNLSEHGLLKDFLKKHNFNPASKYFPQAEAPTLIDEQPLENYLDMEY 76 ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY

FGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACTNHNRFNPQDSSTYQSTSGTVSIT

84 17

77

Matches

Local Similarity

52.9%; 53;

Score 1092.5; DB Pred. No. 1.3e-78; 3; Mismatches 97

DB 1; 97;

Indels Length

9;

Gaps

ω

83

Conservative

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A; Title: Cloning and sequencing of rhesus monkey pepsinogen A cDNA.
A; Reference number: JT0309; MUID:88313666
A; Accession: JT0309
A; Molecule type: mRNA
A; Residues: 1-388 <EVE>
A; Cross-references: GB:M20788; NID:g342274; PIDN:AAA36902.1; PID:g342275
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>F;16-52/Domain: sciivation peptide #status predicted <APT>F:63-388/Product: pepsin #status predicted <APT>F;63-388/Product: pepsin #status predicted <APT>F;94,277/Active site: Asp #status predicted
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C;Date: 30-Jun-1989 #sequence_revision
C;Accession: JT0309
R;Evers, M.P.J.; Zelle, B.; Bebelman, C
Gene 65, 179-185, 1988
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
 RANNQVGLA
                                    RANNLVGLA
                                                                         LPDIVFTINGVQYPLPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                                 MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD
                                                                                                                                                                    DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY
                                                                                                                                                                                                                         PVFDNIWDQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVSVEGYWQISV
                                                                                                                                                                                                                                                            PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY 83
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                                                                                                                                                 DSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGEMVVSCSAISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNRNPASKYFPQTEAPTLIDEQPLENYLDVEY
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                                      387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%;
57.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1085.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-Jun-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 4.8e-78;
smatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pronk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mager,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                              262
                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                          136
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                                                                                                                                                 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Molecule type: protein
A; Mesidues: 41-261, /D', 263-388 < KA3>
C; Comment: This is the major pepsin isozyme in juveniles and adu
C; Comment: Activation is a one-step process.
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; gastric juice; hydrolase; phosp
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 1-15/Domain: activation peptide #status experimental <APT>
F; 63-388/Product: pepsin A 1 #status experimental <ENZ>
F; 94,277/Active site: Asp #status predicted
F; 107-112,268-272,311-344/Disulfide bonds: #status experimental
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F;130/Binding site: phosphate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A92579; A; Accession: A92579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 16-62 < KA2>
R; Kageyama, T.; Takahashi, K.
J. Biol. Chem. 261, 4395-4405,
A; Title: The complete amino ac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Monkey pepsinogens
A;Reference number: A91960;
A;Accession: A91960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: parts of sequence, R;Kageyama, T.; Takahashi, J. Biochem. 88, 9-16, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 202, 205-215, 1991
A;Title: Development-dependent expression
A;Reference number: S19681; MUID:92037645
A;Accession: S19681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pepsin A (EC 3.4.23.1) 1 precursor - Japanese macaque
N,Alternate names: pepsinogen A isozyme 1
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 13-Aug-1986 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Date: S19681; A91960; A92579; A00981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-388 < KAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X59752;
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 379
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hes 210;
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                                                                                                                                                                                                       PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV 262
                                                                                                                                                                                                                                                                                                                                  RANNLVGLA
                                    LPDIVFTINGIQYPVPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                                                            DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY 322
                                                                                                                                                                                                                                                                                   YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203
                                                                                                                                                                                                                                                                                                                                                                                                           IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNLNPASKYFPQAEAPTLIDEQPLENYLDVEY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                              ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY 83
                                                                     MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD 378
                                                                                                              DSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGEMVVSCSAISS
                                                                                                                                                                                    PVFDNIWDQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVSVEGYWQISV 256
                                                                                                                                                                                                                                                              YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1084.5;
Pred. No. 5.7
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ches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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388; 9;

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and PID: 938075

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C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 08-Dec-2000
C;Accession: A00980; PX0023; S02663; F22434; I54252; PX0024
R;Sogawa, K.; Fujii-Kuriyama, Y.; Mizukami, Y.; Ichihara, Y.; Takahashi, K.
J. Biol. Chem. 258, 5306-5311, 1983
A;Title: Primary structure of human pepsinogen gene.
                                                                                                                                                                                                                             A;Gene: GDB:PGA3
A;Cross-references: GDB:119402; OMIM:169710
A;Map position: 11q13.1-11q13.5
A;Introns: 19/2; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein; [F;1-15/Domain: signal sequence #status experimental <SIGN-F;16-388/Product: pepsinogen A 3 #status experimental <APTN-F;16-52/Domain: activation peptide #status experimental <APTN-F;00-388/Product: pepsin A 3, minor variant #status experimental <APTN-F;00-388/Product: pepsin A 3 #status experimental <APTN-F;01-388/Product: pepsin A 3 #status experimental <APTN-F;04,277/Active site: Asp #status predicted
F;130/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Accession: A00980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-15, 'XXX', 19-20, 'X', 22, 'XXX', 25-26, 'X', 28 <ICH>
A; Revers, M.P.J.; Zelle, B.; Peeper, D.S.; Mager, W.H.; Planta,
Hum. Genet. 77, 182-187, 1987
Hum. Genet. 77, 182-187, 1987
A; Title: Molecular cloning of a pair of human pepsinogen A gene
A; Reference number: 154252; MUID:88006181
A; Accession: 154252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 16-68 < FOL>
R; Ichihara, Y; Sogawa, K.; Ta
J. Biochem. 98, 483-492, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 241, 69-72, 1988
A;Title: Activation of human pepsinogens.
A;Reference number: S02663; MUID:89065108
A;Accession: S02663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 16-100 < ATH>
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A; Residues: 1-388 <SOG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, A;Reference number: A22434; MUID:86059312
A;Accession: F22434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Foltmann, B. FEBS Lett. 241,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Athauda, S.B.P.; Tanji, M.;
J. Biochem. 106, 920-927, 1989
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A; Residues: 1-27, 'f', 29-73 < RES>
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                                                                                                                             Query Match
Best Local
                                                                                                          Matches
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19
                                                   30
                                                                                                                             Local Similarity
                                                 RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQYFG 85
  KVPLIRKKSLRRTLSERGLLKDFLKKHNLNPARKYFPQWEAPTLVDEQPLENYLDMEYFG
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                                                                                                                             52.4%;
56.7%;
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                                                                                                       52;
                                                                                                     Score 1082.5;
Pred. No. 8.2e
52; Mismatches
                                                                                          5; DB 1;
3.2e-78;
5.2e-98;
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                                                                                                     9;
                                                                                                     Gaps
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KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145

KVPLIRKKSLRRTLSERGLLKDFLKKHNLNPARKYFPQWEAPTLVDEQPLENYLDMEYFG

78

TIGIGTPAQDFTVLFDTGSSNLWVPSVYCSSLACTNHNRFNPEDSSTYQSTSETVSITYG

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A;Cross-references: GDB:119483; OMIM:169720
A;Map position: 11q13-11q13
A;Matrons: 19/1; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; phosphoprotein; protein digestion; zymoge
F;I-15/Domain: signal sequence #status experimental <STO>
F;16-59/Domain: activation peptide #status experimental <APT>
F;63-388/Product: pepsin A 4 #status predicted <MAT>
F;94,277/Active site: Asp #status predicted
F;107-112,268-272,311-344/Disulfide bonds: #status predicted
F;107-112,268-272,311-344/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: type: DNA
A; Residues: 1-27, 'F', 29-388 <EVE>
A; Note: the authors translated the codon TTC
A; Note: the Sodawa, K.; Takahashi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: B30142; E22434
R;Evers, M.P.J.; Zelle, B.; Bebelman, J.P.; van Beusechem, V.; Kraakman, L.; Genomics 4, 232-239, 1989
A;Title: Nucleotide sequence comparison of five human pepsinogen A (PGA) gene A;Reference number: A91627; MUID:89233110
A;Accession: B30142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Isolation of human, swine, and rat prepepsinogens A;Reference number: A22434; MUID:86059312 A;Accession: E22434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pepsin A (EC 3.4.23.1) 4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 20-Aug-1994 #text_change 29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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A; Residues: 1-15, 'XXX', 19-20, 'X', 22, 'XX', 25-26, 'X', 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Ichihara, Y.; Sogawa, K.;
J. Biochem. 98, 483-492, 198
                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: PGA4
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                                                    Matches
                                                                      Query Match
Best Local
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30 RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQYFG 85
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                                                      209;
                                                                        Similarity
                                                      Conservative
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56.6%;
                                                      53;
                                                    Pred. No. 1.20
3; Mismatches
                                                                        Score 1080.5; DB Pred. No. 1.2e-77
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J. Biochem. 106, 920-927, 1989
A;Title: A comparative study on the NH2-terminal amino acid sequences and A;Reference number: px0023; MUID:90130402
A;Accession: px0027
A;Molecule type: protein
A;Residues: 16-100 <ATH>
A;Molecule type: protein
A;Residues: 16-60 <ATH>
A;Molecule type: protein
A;Residues: 16-60 <ATH>
A;Molecule type: protein
A;Residues: 16-60 <ATH>
A;Molecule type: protein
A;Residues: 16-100 <ATH>
A;Molecule type: protein
A;Residues: 16-100 <ATH>
A;Molecule type: protein
A;Residues: 16-100 <ATH>
A;Molecule type: protein
A;Reference number: A22434; MUID:86059312
A;Accession: A22434
A;Molecule type: protein
A;Residues: 1-15,'xxx',19-20,'x',22,'xx',25-26,'x',28 <ICH>
C;Genetics:
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R;Bank, R.A.; Cru
Rott. 238,
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N;Alternate names: pepsinogen 5
C;Species: Homo saplens (man)
C;Date: 07-Jun-1990 #sequence_revision 20-Aug-1994 #text_change 29-Aug-1997
C;Accession: A30142; S02664; S02542; PX0027; PX0025; PX0026; A22434
R;Evers, M.P.J; Zelle, B; Bebelman, J.P.; van Beusechem, V.; Kraakman, L.; Hof Genomics 4, 232-239, 1989
A;Title: Nucleotide sequence comparison of five human pepsinogen A (PGA) genes: A;Accession: A30142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Foltmann, B., 69-72, 1988
FEBS Lett. 241, 69-72, 1988
A;Title: Activation of human pepsinogens.
A;Reference number: S02663; MUID:89065108
A;Accession: S02664
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 16-58 < BAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S02542; MUID:89005649 A; Accession: S02542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Bank, R.A.; Crusius, B.C.; FEBS Lett. 238, 105-108, 1988
A; Title: Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 16-68 < FOL>
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A; Residues: 1-27, 'F', 29-388 <EVE>
A; Cross reference: GB: M26025
A; Note: the authors translated the
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F;1-15/Domain: signal sequence #status predicted <SIG>F;16-388/Product: pepsinogen A 4 #status experimental <PPT>F;16-62/Domain: activation peptide #status experimental <APT>F;63-388/Product: pepsin A 4 #status experimental <ENZ>F;38-99/Cleavage site: Leu-Lys (pepsin) #status experimental F;62-63/Cleavage site: Leu-Ile (pepsin) #status experimental

Leu-Lys (pepsin) Leu-Ile (pepsin)

C; Superfamily: pepsin
C; Keywords: aspartic proteinase;

gastric juice;

hydrolase; phosphoprotein;

protein

predominantly a o

A;Cross-references: EMBL:X59753; NID:g38070; PIDN:CAA42425.1; PID:g38071 A;Note: parts of sequence, including amino ends of pepsinogen and activation C;Comment: This is a minor component of pepsin at all post-partum stages. C;Comment: Although two-step activation is observerd, activation is predomina

Eur. J. Biochem. 202, 205-215, 1991 A; Title: Development-dependent expression A; Reference number: S19681; MUID:92037645

of

isozymogens

of monkey

pepsinogens

st

A; Molecule type: mRNA A; Residues: 1-388 < KAG> A; Reference number: A; Accession: S19682

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pepsin A (EC 3.4.23.1) 4 Prevent Pepsin A (EC 3.4.23.1) 4 Prevent Pepsin A isozyme 4 N;Alternate names: pepsinogen A isozyme 4 C;Species: Macaca fuscata (Japanese macaque) C;Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 C;Accession: S19682; S16065 C;Accession: K; Koiwai, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 11q13-11q13
A;Introns: 19/1; 73/3; 113/1; 152/3; 219/2; 258/2; 306/3; 339/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; phosphoprotein; prote
F;1-15/Domain: signal sequence #status experimental <SIG>
F;16-388/Product: pepsinogen A 5 #status experimental <ZYM>
F;60-388/Product: pepsin A 5, minor variant #status experimental
F;63-388/Product: pepsin A 5 #status experimental <MAT>
F;94,277/Active site: Asp #status predicted
F;130/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDB: PGA5
                                                                                                                                                                                                                                                                                                         PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGE-----VASVPLTNYLDSQY
                                                                                                                                                                           RANNQVGLA
                                                                                                                                                                                              RANNLVGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVPLIRKKSLRRTLSERGLLKDFLKKHNLNPARKY--FPQWKAPTLVDEQPLENYLDMEY
                                                                                                                                                                                                                                                                                                                                                                          PVFDNIWNQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVTVEGYWQITV
                                                                                                                                                                                                                                                                                                                                                                                                                                           YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 52.3%; al Similarity 56.6%; 209; Conservative
                                                                                         3.4.23.1) 4 precursor - Japanese macaque
                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1078.5; DB Pred. No. 1.7e-77 Pred. No. 1.7e-77 Pred. Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                         #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
J. Biochem. 129, 147-153, 2001
A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens A;Reference number: JC7573; MUID:21064922; PMID:11134969
A;Contents: Stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;94,277/Active site: Asp *status predicted F;107-112,268-272,311-344/Disulfide bonds: *status predicted F;130/Binding site: phosphate (Ser) (covalent) *status 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: DDBJ:AB045380
A;Accession: PC7119
A;Accession: PC7119
A;Mccession: PC7119
A;Mccession: PC7119
A;Mccession: PC7119
A;Mccession: PC7119
A;Mccession: PC70mment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pepsinogen A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C;Accession: JC7574; PC7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
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A; Residues: 1-384 <IKU>
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Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 ;Superfamily: pepsin
;Keywords: stomach; zymogen
                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                      VKVPLRKGESFRNRPQRLGLLGDYLKKNPYNPASKYFPTLAQSSAETLQNYMDIEYYGT 75
                                                                                                                                                              ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFGEVASVPLTNYLDSQYFGK 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGTIGIGTPAQNFTVVFDTGSSNLWVPSVYCYSLACMDHNLFNPQDSSTYRATSKTVSIT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANNQVGLA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt YGTGSMTGILGYDTVKYGGISDTNQIFGLSETEPGFFLYFAPFDGILGLAYPSISSSGAT}
IYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                            52.0%; Score 1074; DB 2; 54.6%; Pred. No. 3.8e-77; tive 64; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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Pred. No. 2.9e-77;
2; Mismatches 99; I
                                                                                                                                                                                                                                                                                                           Length 384;
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δÃ Qy 밁 δÃ В Qy В 뮹 멍 Qy 136 147 256 266 196 DNMWSQGLIPQNLFSVYLSSDGQTGSYVLFGGVDNSYYSGSLWWVPLTAETYWQITLDSV 207 76 GSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF VVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFDRAN 381 TISGYVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPT 325 NLVGLA 387 SINGQVIACSQSCQAIVDTGTSLMTGPSTPIANIQNYIGASQDSNGQYVINCNNISNMPT GSMSGFLGYDTLQVGNIQISNQMFGLSESEPGSFLYYSPFDGILGLAFPSIASSQATPVF 195 ISIGTPPQEFTVIFDTGSANLWVPSVYCSSQACSNHNRFNPQQSSTFQATNTPVSIQYGT 135 IVFTINGVQYPLSPSAYVRQNQQGCSSGFQAMNLPTNSGDLWILGDVFIRQYFTVFDRAN 255 315 265

Search completed: July 31, 2002, 09:21:41 Job time: 333 sec

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on:
          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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InterPro; IPR001461; Pepsin.
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MEDLINE-90356410; PubMed-2117748;
Pungecar J., Strukelj B., Gubensek F.,
"Complete primary structure of lamb precona.";
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                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 18:4602-4602(1990).

-I- FUNCTION: CHYMOSIN IS SYNWHESIZED IN THE MUCOSA CONTROL THE ENZYME HYDROLYZES CASEIN TO PARACASEIN.

-I- CAYALYTIC ACTIVITY: Broad specificity similar to Clots milk by cleavage of a single bond in casein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNLVGLAKAI 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
recursor (EC 3.4.23.4) (Preprocenni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                         CAA37209.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Eutel Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.4%;
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Pred. No. 5.2e-140;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Preprorennin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     preprochymosin
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                                                                                                                                                                                                                                                                                                                                                                                 IN THE MUCOSA OF
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                                                                                      http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                       A1;
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                                                                                                                                                      igh a collaboration - EMBL outstation - strictions on its
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chain)
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CHYM_CALJA
ID CHYM_CALJA
ID CHYM_CALJA
AC Q9N2D2;
DT 16-CCT-2001
DT 16-CCT-2001
DT 01-MAR-2002
DE Chymosin pre
GN CYM.
OS Callithrix:
OC Enkaryota; POC Mammalia; EN
OC Mammalia; EN
OC MOBI_TaxID=6
RN [1]
RP SEQUENCE FR
RP SEQUENCE FR
RP REGULATION.
RC TISSUE-Gast
RX MEDLINE-2021;
RX MEDLINE-2021;
RX Kageyama T.;
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Best Local S
Matches 345
                                                                                                    Q9N2D2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
01-MAR-2002 (Rel. 41, East annotation
SEQUENCE FROM N.A.
REGULATION.
TISSUE=Gastric muc
MEDLINE=20250834;
Kageyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                       Chymosin precursor CYM.
Callithrix jacchus
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SIGNAL
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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                                                                                                                                                                                                                                                                                    TVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 Similarity
345; Conserv
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                                                                        ; Metazoa;
Eutheria;
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308
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                    mucosa
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          PubMed=10788784
                                                                      (Common marmoset); Chordata; Crania; Primates; Platyr
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58
381
92
274
110
269
341
                                    SEQUENCE
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93.2%;
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CHYMOSIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1829; D
Pred. No. 1.9e
13; Mismatches
                                     OF,
                                                                      Craniata; Vertebrata; Euteleostomi; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Digestion;
                                     17-26,
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                                                                                                          (Preprorennin).
                                                                                                                                                       381
                                                                                                                    update)
                                      FUNCTION,
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..9e-132;
nes 12;
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                                      AND
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Query Match
Best Local Similarity
Matches 301; Conser
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ACT_SITE
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB038386; BAA90873.1;
InterPro; IPR001969; Asp_pro
InterPro; IPR001461; Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: Hydrolyses a variety of proteins.
-I- CATALTIC ACTIVITY: Broad specificity similar to clots milk by cleavage of a single bond in casein -I- ENZYME REGULATION: Inhibited by pepstatin.
-I- SUBUNIT: Monomer (By similarity).
-I- DEVELOPMENTAL STAGE: Expressed in adult, not neon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evolution.";
J. Biochem. 127:761-770(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primi; Provozo, Pepsin.
PRIMIS; PRO0792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
PROSITE; PS00141; ASP_PROTEASE; Digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00026; asp; 1
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MISCELLANEOUS: The optimal pH is around SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTIC ASPARTYL PROTEASES
                           AVTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLD 80
                                                                                                                                                              YSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQF
                                                                                                                                                                                                                           SQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPL 140
NNLVGLAKAI 390
                                                                                                                                                                                                                                                                    CQYFGKIYIGTPPQEFTVVFDTGSSDLWVPSVYCNSVACQNHHRFDPSKSSTFQNMDKSL 131
                                                                                                                                                                                                                                                                                                                               ALSQASGIVRIPLHKGKSLRRALKERGLLEDFLKNHQHAVSRKHSNSREVASEFLTNYLD 71
                                                                                                                                                  YSVPVFDNMMDRHLVAQDLFSVYMSRNEQGSMLTLGAIDPSYYTGSLHWIPVTVQEYWQF
                                                                                                                                                                                                           SIQYGTGSMQGLLGYDTVTVSSIVDPHQTVGLSTQEPGDVFTYSEFDGILGLAYPSLASE
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58
381
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284
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                                                                                                                                                                                                                                                                                                                                                                                                      77.8%;
81.4%;
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Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹,
                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                        Score 1605; DB 1;
Pred. No. 2.4e-115;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
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C5820C74C97BB96B C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gastric juice;
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A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 381;
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MBL outstation -
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                                                                                       311
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RESULT 4
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DISULFID
SEQUENCE
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CHAIN
MOD_RES
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                       Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPA_CALJA
Q9N2D4;
                                                                                                                                                                                                                                        PROSITE; PS00141;
                                                                                                                                                                                                                                                      Pfam; Pf00026; a PRINTS; PR00792;
                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                           This
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-!- FUNCTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kageyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Callithrix.
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                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                         InterPro; IPR001969; Asp_protease
InterPro; IPR001461; Pepsin.
                                                                                                                                                                                                                                                                                                EMBL; AB038384; BAA90871.1;
                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20250834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372
18
                                           Local Similarity
nes 215; Conser
                     30
                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Shows particularly broad specificity; involving phenylalanine and leucine are preferralso cleaved to some extent.

CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, ENZYME REGULATION: Inhibited by pepstatin.

MISCELLANEOUS: The optimal ph is around 2.

SIMILARITY: BELONGS TO PEPFIDASE FAMILY A1; ALS EUKARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNLVGLAKAI 381
                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         World monkey
KVSLIKKKSLRKNLIEHGLLKDFLKNNTLDPASKYFPQGEAATMIANQPLVNYLDMEYFG
             RIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGE----VASVPLTNYLDSQYFG 85
                                                                                                                                                                                                                   Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               m. 127:761-770(2000)
                                                                                                                                                                                                                              Aspartyl
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62
129
93
276
106
267
267
310
                                             Conservative
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                                                                                                                                                                                                                                                       PEPSIN
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of enzymatic
                                                                                                                                                                                                                                          ASP_PROTEASE;
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61
387
129
93
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111
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                                                                                                     41563
                                                      53.7%;
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Last annotation updat
C 3.4.23.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                     WW;
                                             49;
                                                                                                  ACTIVATION PEPTIDE (
PEPSIN A.
PHOSPHORYLATION (BY
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QF,
                                          Score 1108.5; DB Pred. No. 1.9e-77; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A and C, and properties, o
                                                                                                                                                                                                                              Digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specificity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                              Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d prochymosins. Purification, cDNA cloning, and molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ificity; although bonds preferred, many others
                                             94;
                                                                                                                                                                       (BY SIMILARITY)
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                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                            ALSO KNOWN
                                                                                                     CRC64;
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                                                                  Length
                                                                                                                                                                                              SIMILARITY)
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     CHAIN
ACT_SITE
ACT_SITE
DISULFID
                                                                                                          Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Embryonic pepsinogen precursor (EC 3.4.23.-).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88227903; PubMed-3131317;
Hayashi K., Agata K., Mochii M., Yasugi S., Eguchi G., Mizuno T.;
"Molecular cloning and the nucleotide sequence of cDNA for embryonic chicken pepsinogen: phylogenetic relationship with prochymosin.";
J. Blochem. 103:290-296(1988).
-I- DEVELOPMENTAL STAGE: SPECIFICALLY SECRETED DURING THE EMBRYONIC PERIOD IN THE CHICKEN PROVENTRICULUS (GLANDULAR STOMACH).
                                                                                                                          PRIME: PROOF2; PEPSIN
PRIMES: PROOF2; PEPSIN
PROSITE; PS00141; ASP_PROTEASE; 2.
PROSITE; PS00141; ASP_PROTEASE; Digestion;
                                                                                                                                                                                                                                                                                                                                                 EMBL; D00215; BAA00153.1; PIR; A41443; A41443.
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPE_CHICK P16476;
                                                                                                                                                                                                                                       InterPro; IPR001969;
InterPro; IPR001461;
                                                                                                                                                                                                                                                                                               MEROPS; A01.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGSMTGILGYDTVQVGGIADTNQIFGLSETEPGSFLYYSPFDGILGLAYPSISSSGATPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG
                                                                                                                                                                                                                    PF00026; asp;
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                                                                                                                                                                                                                                                                                                                              P00794;
  ; Aspartyl protease;

1 16 P

17 383 E

94 94 B

276 276 B

107 112 B
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POTENTIAL.
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BY SIMILARITY.
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                                                                                                                                Signal; Glycoprotein
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RESULT 6
PEP2_W
PEP2_W
ID PEP2_W
AC P27677
AC P2767
AC P26767
AC P2767
AC P2767
AC CC -i- DE CC 
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Pepsinogens and structural differences between them.";

EUR. J. BLOCHEM. 202:205-215(1991).

2-i- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOU INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERED, MAN ALSO CLEAVED TO SOME EXTENT.

2-i- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-.

3-i- DEVELOPMENTAL STAGE: PEP A-2 IS PREDOMINANT AT THE 4-N-

DEP A-3 IS PREDOMINANT AT FETAL STAGES.

3-i- PTM: PEP A-2 IS PHOSPHORYLATED, BUT NOT PEP A-3.

3-i- PTM: PEP A-2 IS PHOSPHORYLATED, BUT NOT PEP A-3.

3-i- PTM: PEP A-2 IS PHOSPHORYLATED, BUT NOT PEP A-3.

3-i- PTM: PEP A-2 IS PHOSPHORYLATED, BUT NOT PEP A-3.

3-i- PTM: PEP A-3 IS PRESULT OF THE RELEASE OF A 47 AA ACTIVED IN THE PEPSINOGEN IS CONVERTED TO CORRESPONDING PEPSINOGEN PEPSINOGE
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01-AUG-1992 (Rel. 23, Last sequence update)
10-AUG-1992 (Rel. 39, Last annotation update)
10-AUX-2000 (Rel. 39, Last annotation update)
10-AUX-2000 (Rel. 23, Created)
10-AUX-2000 (Rel. 23, Last sequence update)
10-AUX-2000 (Re
                                                                                                                                                                                                                                                                                                                                                            TISSUE=Gastric mucosa; MEDLINE=92037645; PubMed=1935977;
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NCBI_TaxID=9543;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopith
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PIR; S19684; S19684.
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Pred. No. 3.2e-76;
3; Mismatches 97;
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PGA.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                 prOSITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Digestion;
                                                                                                                                                                                                                                                                                                           PRINTS; PR00792;
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001969; Asp_protease
InterPro; IPR001791; Laminin_G.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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HSSP; P00790; 1P
MEROPS; A01.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (SEP-1988) to the EMBL/GenBank/DDBJ databases. FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTH INVOLVING PHENVLALANINE AND LEUCINE ARE PREFERRED, PALSO CLEAVED TO SOME EXTENT.

CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEUSIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a c
                        ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY
IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNRNPASKYFPQTEAPTLIDEQPLENYLDVEY
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, Zelle B., Bebelman J.P., Pr
Eriksson A.W., Frants R.R.;
sequencing of rhesus monkey
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                                                                                                                           MW.
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                                                   Score 1085.5;
Pred. No. 1.1e
51; Mismatches
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Catarrhini; Cercopithecidae;
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PHOSPHORYLATION
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                                                      .5; DB 1;
1.1e-75;
hes 98;
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01-AUG-1992 (Rel. 3

30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                         "The complete amino acid sequence of mon J. Biol. Chem. 261:4395-4405(1986).
-!- FUNCTION: SHOWS PARTICULARLY BROAD SINVOLVING PHENYLALANINE AND LEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-81006790; PubMed-6773933; Kageyama T., Takahashi K.; **Monkey pepsinogens and pepsins. IV. activation peptide segment of Japanes J. Blochem. 88:9-16(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                        MEDLINE=86168132;
Kageyama T., Takal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pepsinogens and
Eur. J. Biochem.
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MEDLINE=92037645; PubMed=1935977;
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NCBI_TaxID=9543;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 16-62.
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MISCELLANEOUS: EACH PEPSINOGEN IS CONVERTED TO CORRESPONDING PEPSIN AT PH 2.0 IN PART AS A RESULT OF THE RELEASE OF A 47 PEPSIN AT PH 2.0 IN PART AS A RESULT OF STEPWISE PROTECTION SEGMENT AND IN PART AS A RESULT OF STEPWISE PROTECTION OF THE PRO
                                                                                                                CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-.
DEVELOPMENTAL STAGE: PREDOMINANT AT THE JUVENILE & ADULT STAGES.
MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED E
HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                          ALSO CLEAVED TO SOME EXTENT
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RANNQVGLA
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                                                                                                                                                                                                                                                                                                                          Takahashi K.;
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23, Last sequence update)
39, Last annotation update)
sor (EC 3.4.23.1) (Pepsin III-3).
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                                                                                                                                                                                                                                                   SPECIFICITY;
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Matches 210; Conser
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PIR; S19681; S19681.
HSSP; P00790; 1PSN.
MEROPS; A01.001; -.
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Hydrolase; Aspartyl protease; Digestion; Stomach; G
Zymogen; Phosphorylation; Multigene family; Signal.
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InterPro; IPR001791; Laminin_G.
InterPro; IPR001461; Pepsin.
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            RANNLVGLA
RANNQVGLA
                                                             MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD
                                                                                                          DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY
                                                                                                                                                            PVFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTV
                                                                                                                                                                                                           YGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSI
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                                               LPDIVFTINGIQYPVPPSAYILQSQGSCTSGFQGMDVPTESGELWILGDVFIRQYFTVFD
                                                                                             DSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGEMVVSCSAISS
                                                                                                                                            PVEDNIWDQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVSVEGYWQISV
                                                                                                                                                                                            YGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGAT
                                                                                                                                                                                                                                                                                            IYKVPLVRKKSLRRNLSEHGLLKDFLKKHNLNPASKYFPQAEAPTLIDEQPLENYLDVEY
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41
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107
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311
94
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388
112
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272
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56.9%;
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N -> D (IN REF.
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Pred. No. 1.3e-75;
2; Mismatches 98;
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P00790;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pepsin A precursor (EC 3.4.23.1).
PGA3 AND PGA4 AND PGA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE OF 16-100 (ISOZYMES 2; 3; 3A; 4 AND 5).
MEDLINE-90130402; PubMed=2515193;
Athauda S.B.P., Tanji M., Kageyama T., Takahashi K.;
Athauda S.B.P. anji M., Kageyama T., Takahashi K.;
"A comparative study on the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequences and "A comparative study of the NH2-terminal amino acid sequen
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Sogawa K., Fujii-Kuriyama Y., Mizukami
Primary structure of human pepsinogen
J. Biol. Chem. 258:5306-5311(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human Eukaryota; Metazoa;
EMBL; J00287;
EMBL; J00279;
EMBL; J00280;
                                                                                                                                                                                                                                                    Crystal structure of human pepsin and its complex verotein Sci. 4.960-972(1995).

-I- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY;
INVOLVING PHENVILALANINE AND LEUCINE ARE PREFERRIALSO CLEAVED TO SOME EXTENT.
-I- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-,
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO EUKARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and determination of the primary structures NH2-terminal signal sequences.";
J. Biochem. 98:483-492(1985).
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Hoffer M.J.V., Pronk J.C.,
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MEDLINE=86059312; PubMed=2415509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=95392399; PubMed=7663352;
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Fujinaga M., Chernaia M.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89065108;
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                                                                                                                                                  European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                               M.N.G.;
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  ; AAA98529.1;
; AAA98529.1;
; AAA98529.1;
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:69-72(1988).
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  /FTId=VAR_006487.
C9CB89BA08F4D78B CRC64;
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                                                                                                                          between
the Euro
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                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Gastric mucosa;
MEDLINE-92037645; PubMed-1935977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercopithecinae; Macaca.
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P27678;
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 s: x59753;
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s: S19682; s
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InterPro; IPR001969; Asp_pro
InterPro; IPR001791; Laminin
InterPro; IPR001461; Pepsin.
            SEQUENCE FROM N.A.
MEDLINE-88313677; PubMed-3044927;
Tsukagoshi N., Ando Y., Tomita Y.
Sasaki T., Yamagata H., Udaka S.,
                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSTITE: PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Digestion; Stomach; Tymnonen; Multigene family; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITRIPLYKGKSLRKALKEHGLLEDFLOKOQYGISSKYSGFGEVASV----PLTNYLDSQY
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Tomita Y., Uchida R., Takemura T
Udaka S., Ichihara Y., Takahashi
d expression in Escherichia coli
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ACTIVATION PEPTIDE.
PEPSIN A-4.
BY SIMILARITY.
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52; Mismatches
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No. 6.46
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"N-terminal sequence of swine pepsinogen and pepsin. The site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and determination of the primary structures NH2-terminal signal sequences.";
3. Blochem. 98:483-492(1985).
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MEDLINE-69054241; PubMed=4881358;

MEDLINE-F69054241; PubMed=4881358;

Ong E.B., Perlmann G.E.;

"The amino-terminal sequence of porcine
J. Biol. Chem. 243:6104-6109(1968).
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SEQUENCE OF 16-134.
SEQUENCE OF 16-134.
PubMed=4584879;
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"Complete amino acid sequence of hog
"EBS Lett. 43:207-211(1974).
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bayliss R.S., Knowles J.R., Wybrandt G.F. "An aspartic acid residue at the active and sequence of the heptapeptide."; Biochem. J. 113:377-386(1969).
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                                                                                                                                                                                                                     MEDLINE=91017500; PubMed=2217:
Abad-Zapatero C., Rydel T.J.,
"Revised 2.3 A structure of po"
                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90317821; pubMed=2115088;
Cooper J.B., Khan G., Taylor G., Tickle I.J., Blundell T.L.;
"X-ray analyses of aspartic proteinases. II. Three-dimensional
structure of the hexagonal crystal form of porcine pepsin at 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY
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MEDLINE=86059312; PubMed=
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                               MEDLINE=91278095; PubMed=2056534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  resolution.";
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                                                                         -RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
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                                                                                                                                                                                              n 2.3
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                                                                                                                                                   8:62-81(1990)
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Read R.J.,
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n. III. Amino acid sequence
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PIR; A00982; PEPG.
PIR; B22434; B22434.
PIR; JT0307; JT0307.
PDB; 3PEP; 15-APR-90.
PDB; 4PEP; 15-JAN-91.
PDB; 5PEP; 15-JUL-90.
PDB; 1PSA; 31-JAN-94.
PDB; 2PSG; 15-JAN-93.
MEROPS; A01.001; --
PEROPS; A01.001; --
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MEDLINE=92279205; PubMed=1594574;
Hartsuck J.E., Koelsch G., Remington S.
"The high-resolution crystal structure
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InterPro; IPR001791; Laminin_G.
InterPro; IPR001461; Pepsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00026; asp;
                                                                                                                                                                                      STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO END.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALSO CLEAVED TO SOME EXTENT. CATALYTIC ACTIVITY: PREFERENTIAL PTM: MINOR AMOUNTS OF THE ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WWW="http://www.worthington-biochem.com/manual/P/PM.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way find and this citemant if the content is a content in the content is the content in the content is the content is the content in the content i
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    PEPSIN.
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    N -> D (IN REF. 3 AN
DS -> SD (IN REF. 2).
Q -> E (IN REF. 2).
MISSING (IN REF. 2 A
S -> Q (IN REF. 5).
N -> D (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION
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E ARE PREFERR
                                                                                                                                                                                                                                                                                                                                                                             (IN REF. 2).
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124
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Pred. No. 1.7e-74;
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RESULT

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30-MAY-2000 (Rel. 39, Last annotation update)
Pepsin A).
Pepsin A).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001969; /
InterPro; IPR001461; /
Pfam; PF00026; asp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; A01.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kageyama T., Tanabe K., Koiwai O.; "Structure and development of rabbit pepzymogens, nucleotide sequences of CNAs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=91009127;
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01-DEC-1992
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HSSP; P00791; 1PSA.
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Biol. Chem. 265:17031-17038(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ALSO CLEAVED TO SOME EXTENT.

CAPALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LEU-
DEVELOPMENTAL STAGE: PEPSINOGENS IN GROUP I, II, AND III WHERE THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.

MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN EUKARYOTIC ASPARTYL PROTEASES FAMILY.
SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                                                                                                     VFDNMMNRHLVAQDLFSVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVD
                                                                                                                                                                             GTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIP
                                                                                                                                                                                                                                                                                                                           VHKVPLVRKKSLRKNLIEKGLLQDYLKTHTPNLATKYFPKETFASVSTESLENYLDAEYF
                                                                                                                                                                                                                                                                                                                                                  ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY---SGFGEVASVPLTNYLDSQYF
: ::|| : ||||| | | |||:||:||
                                                                                                                                                    {\tt GTGSMTGILGYDTVKVGNIEDTNQIFGLSKTEPGITFLVAPFDGILGLAYPSISASDATP}
                                                               VFDNMWNEGLVSEDLFSVYLSSNGEKGSMVMFGGIDSSYYTGSLNWVPVSHEGYWQITMD
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PS00141; ASP_PROTEASE;
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(Rel. 39,
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be K., Koiwai O.
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MEDLINE=91009127; PubMed=2129536;
Kageyama T., Tanabe K., Koiwai O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucleotide sequences of cDNAs, molecular evolution, and {\tt z}
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Pfam; PF00026; asp;
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                                                                                         Local Local 203;
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Biol. Chem. 265:17031-17038(1990).

FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; AL
INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED,
ALSO CLEAVED TO SOME EXTENT.

CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE PHE-, LE
DEVELOPMENTAL STAGE: PEPSINOGENS IN GROUP I, II, A
THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.

MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORMONES AND RELATED SUBSTANCES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1;
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
; D38302; D38302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANNLVGLAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDIVETINNVQYPLPASAYILKEDDDCLSGFDGMNLDTSYGELWILGDVFIRQYETVFDR
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                                                            ANNQVGLAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSEN----HSQKWILGDVFIREYYSVFDR
             GKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHY
                                           VHKVPLVRKKSLRKNLIEKGLLQDYLKTHTPNPATKYFPKETFATVSTESLENYLDAEYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00790;
                                                                                                                                                                                                                                                                                                                                                                                                                                   A01.001;
                                                                                                                                                                                                                                                                                                                                                                       PR00792;
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                            Signal;
16
60
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93
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106
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310
387
                                                                                                                                                                                                                                                                                                                                               Aspartyl
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                       PEPSIN
                                                                                                                                                                                                                                                                                                                               Phosphorylation; Multigene family
                                                                                                                                                                                                                                                                                                                                           protease; Digestion; Stomach; Gastric juice;
                                                                                                                   50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Asp_protease
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                                                                                                    57;
                                                                                                                                                                                       ACTIVATION PEPTIDE.

PEESH II-4.

PHOSPHOKYLATION (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                  Score 1037;
Pred. No. 5
                                                                                                                                                                            21ADD07782A89585 CRC64;
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                                                                                                    Mismatches
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                                                                                                                ; DB 1;
5.5e-72;
ALSO KNOWN
                                                                                                                              Length
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                                                                                                     Indels
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P27822
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                                                         InterPro; IPR001969; Asp_proteas
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSTIE; PS00141; ASP_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91009127; PubMed=2129536;
Kageyama T., Tanabe K., Koiwai O.
                                                                                                                                                                                                                                                                                                 EMBL; M59237; AAA853
PIR; E38302; E38302.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEP3_RABIT
                                   Hydrolase;
                                                                                                                                                                                                                                    MEROPS; A01.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSO CLEAVED TO SOME EXTENT. CATALYTIC ACTIVITY: PREFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: SHOWS PARTICULARLY BROAD S INVOLVING PHENYLALANINE AND LEUCINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression during development." iol. Chem. 265:17031-17038(1990)
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                                                                                                                                                                                                                                                                            P00791;
e; Aspartyl protease; Dige
Signal; Phosphorylation;
                                                                                                                                                                                                                                                                            4PEP.
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S IN GROUP I, II,
E POSTNATAL STAGE.
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                                   Stomach;
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                                       Gastric juice;
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Best Local Similarity
Matches 199; Conserv
                                        Rageyama T., Tanabe K., Koiwai O.;

"Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucleotide sequences of cDNAs, molecular evolution, and gene expression during development.";

J. Biol. Chem. 265:17031-17038(1990).

-I- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONI INVOLVING PHENYLALANIME AND LEUCINE ARE PREFERRED, MANY OTHER ALSO CLEAVED TO SOME EXTENT.
                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolac
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                 PEP2_RABIT P27821;
                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pepsin II-2/3 precursor (EC 3.4.23.1) (Pepsin
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ALSO CLEAVED TO SOME EXTENT.
CATALYTIC ACTIVITY: PREFERENTIAL
DEVELOPMENTAL STAGE: PEPSINOGENS
THE PREDOMINANT ZYMOGENS AT LATE
MISCELLANEOUS: THE EXPRESSION OF
HORMONES AND RELATED SUBSTANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                               SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                                                                                                                                                                                                               ANNLVGLAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                     SITMDGETIACADSCQAIVDTGTSLLAGPTSAISNIQSYIGASENSDGEMIVSCSSMYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFDNMWNEGLVSEDLFSVYLSSDDESGSVVMFGGIDSSYYTGSLNWVPVSYEGYWQITLD
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PEPSIN III.
PHOSPHORYLATION (POT
BY SIMILARITY.
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Pred. No. 9.
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                   L CLEAVAGE PHE-, LI
S IN GROUP I, II, I
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            PEPSINOGEN GENES
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SIGNAL
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PIR; C38302; C38302.
HSSP; P00790; 1PSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001969;
InterPro; IPR001461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00026; asp; 1. PRINTS; PR00792; PEPSIN
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                                                                                                        SVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM
                                                                                                                                                         VFDNMMNRHLVAQDLESVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVD
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ANNQLGLAAAV
                        ANNLVGLAKAI
                                                         PTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSEN----HSQKWILGDVFIREYYSVFDR
                                                                                              SYSINGETIACADSCQAIVDTGTSLLTGPTSAISNIQSYIGASKNLLGENVISCSAIDSL
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                                             PDIVFTINGIQYPLPASAYILKEDDDCTSGLEGMNVDTYTGELWILGDVFIRQYFTVFDR
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PHOSPHORYLATION (POT
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                    Score 1029;
Pred. No. 2.
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Search completed: July 31, 2002, 09:25:11 Job time: 233 sec

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Q28950 sus scrofa
Q9jjx1 rattus norv
Q28075 bos taurus
Q9gmy6 canis famil
Q9dec4 rana catesb
Oggmy8 sorex unqui
O29080 sus scrofa
O99m97 rhinolophus
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Best Local Similarity
Matches 357; Conserv
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
Asparty1 protease; Hydrolase.
SEQUENCE 366 AA; 40498 MW; 279BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9N1P5 PRELIMINARY; PRT; 366 AA.
Q9N1P5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Batish V.K., Mukhopadhyay U.K., Mohanty A.K., Grover S., Kuipers O.P.;
Submitted (AUG-199) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY AI; ALSO KNOWN AS THE
EUGRAYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AF177290; AAF27315.1; --
HSSP; P00794; 4CMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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AEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASVPLTNYLDSQYFG 85
                                                                                                                                                                         Conservative
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                                                                                                                                                                Score 1883; DB 6;
Pred. No. 5.7e-150;
3; Mismatches 5;
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Best Local Similarity
Matches 342; Conser
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; Asp; 2.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; UI
SEQUENCE 345 AA; 38034 MW; 390
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01-NOV-1996
01-DEC-2001
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Q27951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1995) to EMBL; U19786; AAA73476.1 HSSP; P00794; 4CMS.
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Tan S.-y., Zhang Y.-y.,
"Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; A01.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos. NCBI_TaxID=9909;
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Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos primigenius (aurochs).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                      146
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                   TGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPV
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Biotechnol.
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                                                                                                                                                                                                                                       Conservative
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93.7%;
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Pepsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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Pred. No. 1e-1
1; Mismatches
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396DECEE2996AlFA CRC64;
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                                                              DPRKSSTFQNLGKPLSIHYG
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Best Local Sim
Matches 309;
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Q9GK11;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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01-MAR-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHYMOSIN PRECURSOR (EC 3.4.23.4).
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus

      PROSITE;
      PS00141;
      ASP_PROTEASE;
      1.

      Aspartyl
      protease;
      Hydrolase;
      Signal.

      SIGNAL
      1
      58
      POTENTIA

      CHAIN
      59
      381
      CHYMOSIN

      SEQUENCE
      381
      AA;
      42082
      MW;
      24BADB

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InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9838;
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191
                                             200
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|LAKAI 345
                                                                                                                                                                                                                                                                                      LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS
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                      EYSIPVFDNMMNRHLYAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQ
                                                                                                                                                                                            DSQYFGKIYIGTPPQEFTVVFDTGSSDLWVPSIYCKSNVCKNHHRFDPRKSSTFRNLGKP
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity 83.3
09; Conservative
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ius) Chymosin
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                                                                                                                                                                                                                                                                                                                                                                                      Score 1670; D
Pred. No. 4.7e
34; Mismatches
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4.7e-132;
hes 28;
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Best Local Similarity
Matches 297; Conserv
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PROPEP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
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Foltmann B., Jensen A.L.,
"A developmental analysis
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PREPROTYMOSIN PRECURSOR (FRAGMENT).
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PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001969; InterPro; IPR001461;
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                       LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS 199
                                                                             LALSQGSGITRVPLRKGKSLRKELKERGLLEDFLQKQPYALSSKYSSFGEVASEPLTNYL
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                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                Score 1601; DB 6; Pred. No. 2.9e-126;
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ACTIVATION PEPTIDE (POTENTIAL).
CHYMOSIN.
; ECA81B78239D2102 CRC64;
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Best Local Similarity
Matches 265; Conser
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SEQUENCE
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROCHYMOSIN PRECURSOR (EC 3.4.23.4).
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
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SIGNAL 1
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EMBL; AJ251688; CAB75983.1;
HSSP; P00794; 4CMS.
MEROPS; A01.006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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FTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDN
                                                                                                                                                                                                                                DSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKP 139
                                                                                                                                                                                                                                                                                                                             KYSVPIFDNMMNRHLVAQDLFSVYMSRNDQGSMLTLGAIDQSYFIGSLHWVPVTVQGYWQ
                                                                      EYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQ
                                                                                                                                      LFVQYGTGSVEGFLAYDTVTVSDIVVPHQTVGLSTEEPGDIFTYSPFDGILGLAYPTFAS
                                                                                                                                                              LSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLAS 199
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PROCHYMOSIN.
; 49F650CC759A5ADC CRC64;
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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01-DEC-2001
CHYMOSIN C.
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Q28075;
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; Asp; 1.
PROSITE; PS00141; ASP_PROTEASE; UN
SEQUENCE 242 AA; 26684 MW; 4EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biochem. 91:1085-1088(1982).
EMBL; J00004; AAA30449.1; -.
HSSP; P00794; 1CMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=FOURTH STOWACH MUCOSA;
MEDLINE=82187915; PubMed=6804449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
Q9GMY6;
01-MAR-2001
                                            Q9GMY6
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"Nucleotide sequence of calf prorennin
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01-MAR-2001 (3
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PEPSINOGEN A.
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PRINTS; PR00792; PEPSINTS;
PROSITE; PS00141; ASP_PROTEASE;
Aspartyl protease; Hydrolase.
SEQUENCE 386 AA; 41551 MW; 5
    Eukaryota;
Amphibia;
                        Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                             Q9DEC4
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InterPro; IPR001791;
InterPro; IPR001461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLASEYSIPVEDNAMNRHLVAQDLESVYMDRNGQE-SMLTLGAIDPSYYTGSLHWVPVTV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VALSECA-IVKVPLVRKKSLRQNLIEHGLLNDFLKNQSPNPASKY--FPQEPTVLATQSL
                                                                                                                                                                                                                                                                                         ROYFAVFDRANNOVGLA
                                                                                                                                                                                                                                                                                                                    REYYSVFDRANNLVGLA
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                                                                                                                                                                                                                                                                                                                                                                             ISCSAINSLPDIVFTINGIQYPLPPSAYILQSQQGCVSGFQGMNLPTASGELWILGDVFI
                                                                                                                                                                                                                                                                                                                                                                                                     IDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSEN----HSQKWILGDVFI
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    Batrachia;
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tion of Insectivora in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.5%;
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    Anura;
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19,
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Last annotation update)
                                                                                                              Created)
      Neobatrachia;
                                                                                          Last annotation update)
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Pred. No. 1.4e-84;
4; Mismatches 96
                           Craniata;
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                                                                                                              sequence update)
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    Vertebrata;
a; Ranoidea;
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      Ranidae;
                        Euteleostomi;
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Best Loc
Matches
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"Molecular Cloning of
Rana catesbeiana.";
Submitted (JUN-2000) t
          SEQUENCE FROM N.A.

Narita Y., Oda S., Takenaka O., Kageyama T.;

"Phylogenetic position of Insectivora inferred of pepsinogen A and C.";
                                                         Suncus murinus (House shrew) (Mu:
Eukaryota; Metazoa; Chordata; Cri
Mammalia; Eutheria; Insectivora;
NCBI_TaxID=9378;
                                                                                                  PGNA.
                                                                                                          PEPSINOGEN A.
                                                                                                                                                  Q9GMY9;
                                                                                                                                                          Q9GMY9
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InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
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1-MAR-2001
1-DEC-2001
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hes 213;
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                                                                                                                                                                                                                    DVFIREYYSVFDRANNLVGLA
                                                                                                                                                                                                                                                          GEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSEN----HSQKWILG
                                                                                                                                                                                                                                                                                                  PVTVQQYWQFTVDSVTISGYVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQY
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  (AUG-2000)
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Last anno
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Pred. No. 3.9e.
47; Mismatches
                                                                   ) (Musk shrew).
h; Craniata; Vert
70ra; Soricidae;
  EMBL/GenBank/DDBJ databases
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on update)
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                                                                             Euteleostomi;
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Best Local S
Matches 209
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                    "Phylogenetic position of Insectivora inferred of pepsinogen A and C."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ do-i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; EUKARYOTIC ASPARTYL PROTEASES FAMILY.

EUKARYOTIC ASPARTYL PROTEASES FAMILY.
Pfam; PF00026;
                                                                                                                                                                                                                                         SEQUENCE FI
                                                                                                                                                                                                                                                                                                                             Sorex unguiculatus (Long-clawed shrew).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Insectivora; Soricidae;
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PROSITE; PS00141; ASP_PROTEASE;
ASPARTY1 Protease; Hydrolase.
SEQUENCE 387 AA; 41576 MW;
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EMBL; AB047243; BAB11749.1; -.
HSSP; P00790; 1PSN.
InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
                InterPro; IPR001969; Asp_protease
InterPro; IPR001461; Pepsin.
                                                            MEROPS; A01.001;
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Matches

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    PRINTS; PR00792; PEPSIN.

    PROSITE; PS00141; ASP_PROTEASE; 2

    ASPATTYL protease; Hydrolase; Sig

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J. Biol. Chem. 264:4482-4489(1989).
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY.
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
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HSSP; P00791; LPSA.
MEROPS; A01.001; -.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE;
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01-NOV-1996 (TrembLrel.
01-DEC-2001 (TrembLrel.
PEPSINOGEN A PRECURSOR.
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InterPro; IPR001791; Laminin_G.
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                                                                                                                                                 InterPro; IPR001461; Pepsin
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Lin X.-L., Wong R.N.S., Tang J.;
"Synthesis, purification, and active-site mutagenesis
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Best Local S
Matches 208
Query Match 52.7
Best Local Similarity 56.7
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                     01-MAR-2001
01-DEC-2001
PEPSINOGEN A
                                                                                                                             "Phylogenetic position of Insectivora inferred f
of pepsinogen A and C.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ da
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1;
EUGARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AB047245; BABI1751.1;
HSSP; P00790; 1PSN.
                                                     PRINTS; PR00792; PEPSIN.
PROSITE; PS00141, ASP_PROTEASE;
Asparttyl protease: Hydrolase.
SEQUENCE 386 AA; 41591 MW;
                                                                                                                                                                                                                                                                                                         PGNA.
                                                                                                                                                                                                                                                                                                                                                   Q9GMY7;
01-MAR-2001
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          Q9GMY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                Pfam; PF00026; asp;
                                                                                                                                                                                                                                                                  Rhinolophus
                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                Rhinolophus
                                                                                                                                                                                                                                                     NCBI_TaxID=59479;
                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                         InterPro; IPR001969; Asp_protease InterPro; IPR001461; Pepsin.
                                                                                                                                                                                                                                                                                                                                                                                                                               374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGEVASV----PLTNYLDSQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANNLVGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPDIVETINGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS----ENHSQKWILGDVFIREYYSVFD
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                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                       Oda
                                                                                                                                                                                                                                                                                    Metazoa;
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tion of Insectivora inferred
                                                                                                                                                                                                                                                                        Chordata; C:
Chiroptera;
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           52.7%;
56.7%;
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56.4%;
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                                                                                                                                                                                                                                                                                                                               Last
Last
                                                                                                                                                                                                                                                                                                                                                    Created)
Score 1087.5; D
Pred. No. 4e-83;
4; Mismatches
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Pred.
                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostom
a; Microchiroptera; Rhinolophidae;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                      917EE04D3166C3A4
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                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
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                     DB 6;
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                     Length
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                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                            KNOWN
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                      386;
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                                                                                        Query Match
Best Local Similarity
Matches 207; Conser
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
PEPSIN A PRECURSOR (EC 34.23.1)
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GK10;
                                                                                                                                                                                                                                               InterPro; IPR001969; Asp_protease.
InterPro; IPR001461; Pepsin.
InterPro; IPR001461; Pepsin.
InterPro; IPR001461; Pepsin.
Prim; Pr00026; asp; I.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 1.
Aspartyl protease; Hydrolase; Signal.
Aspartyl protease; Hydrolase; Signal.
SIGNAL 1 63
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-GASTRIC MUCOSA;
Kappeler S.R., Farah Z
                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; A01.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for Camel Milk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kappeler S.R., Farah Z., Puhan Z.;
Camel (Camelus dromedarius) Chymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9838;
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                     VTHAAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKY-SGFGEVASV----PLT:|| ::|| | |: ||: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                       P00790; 1PSN.
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390
                                                                                      52.5%;
llarity 55.2%;
Conservative 5
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                                                                                      Score 1084; DB Pred. No. 8e-83; Mismatches
                                                                                                                                                                                                      PEPSIN A.; 7A679DDF946D7F8D CRC64;
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Q9DEC2;
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                                                                                                                                                                                                                                                                    Rana catesbelana.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al; ALSO KNI EUKARYOTIC ASPARTYL PROTEASES FAMILY.
EMBL; AB045380; BAB20798.1; -BBPL/GENBL; AB045380; BAB20798.1; -BSSP; P00790; 1PSN.
HSSP; P00790; 1PSN.
                                                                                                                                                                                         PROSITE; PS00141; ASP_PROTEASE; Aspartyl protease; Hydrolase. SEQUENCE 384 AA; 41888 MW;
                                                                                                                                                                                                                         InterPro; IPR001969; Asp
InterPro; IPR001461; Pep
Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                           Ikuzawa M., Inokucn
"Molecular Cloning
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPSINOGEN A.
 136
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          GSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF
                                         YETVEDRANNQVGLA
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                                                                                                                                   Similarity 54.9
)1; Conservative
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             Inokuchi
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                                                                                                                                                                                                                                                        Asp_protease
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                                                                                                                                    64;
                                                                                                                                  Score 1081; D
Pred. No. 1.4e
64; Mismatches
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                                                                                                                                   ; DB 13;
1.4e-82;
hes 95;
                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
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                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98440813; PubMed=9753645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPSINOGEN A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Aspartyl protease; Hydrolase.
SEQUENCE 382 AA; 42056 MW; C3C7EB8CA4DD3E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001969; InterPro; IPR001461;
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TGSMQGILGYDTVTVSNIVDIQ-QTVGLSTQEPGDVFTYAEFDGILGKAYPSLASEYSIP
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                                                                                                                          KIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYG 145
                                                                                                                                                                                                 IHRVPLKKGKSLRKQLKDHGLLEDFLKKHPYNPASKYHPVLTATESYEPMTNYMDASYYG
                                                                                                                                                                                                                                                                                                  201;
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                                                                                                                                                                                                                                                                                                  Conservative
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Pepsin.
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                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                             Score 1016.5; DB 13; Length 382; 
Pred. No. 3.6e-77; 
7; Mismatches 97; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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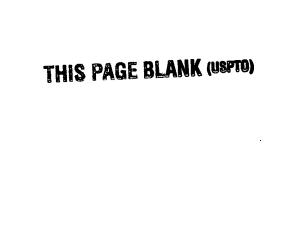
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                                                                                                                     SVTISGYVVACEGGCQAILDTGTSKLYGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYM 323
ANNKVGLS
                  ANNLYGLA 387
                                       PDVTFHINGHAFTLPASAYVLNEDGSCMLGFENMGTPTELGEQWILGDVFIREYYVIFDR
                                                                               RVTVGNKYVACFFTCQAIVDTGTSLLVMPQGAYNRIIKDLGVSSD--GE--ISCDDISKL
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Search completed: July 31, 2002, Job time: 233 sec 09:24:51



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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## ALIGNMENTS

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Sequence 3 from Patent WO0114571.
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VERSION AXO88021
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ORGANISM synthetic construct
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AUTHORS
TITLE
JOURNAL Patent, G., Keon, R. G., Boothe, J. and Shen, Y.
FEATURES
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ORGANISM Synthetic construct
AUTHORS
TITLE
JOURNAL Schen, G., Keon, R. G., Boothe, J. and Shen, Y.
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Location/Qualifiers
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Phaseolus vulgaris. Phaseolus vulgaris PHYBCSP 3502 bp DNA linear PLN 17-JUN-1998 Phaseolis vulgaris beta-type phaseolin storage protein gene, complete cds.
J01263 M13758
J01263.1 GI:3228361

RESULT 2
PHVBCSP
LOCUS
DEFINITION

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GANGAAGTTTGTCTCCATTTATATATATATATATACCCACTTATGTATTATATAGA 31 ttaaggagacataacaattataaaggagaagtttgtatccatttatatattatatac 31 ttaaggagacataacaattataaaggagaagtttgtatccatttatatattatatac 31 ttaaggagacataacaattataaaggagaagtttll	tgaactctcttactc 33	tatttctaatattttagttgatatgtatatgaaagggtact	3241	Qy
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Proc. Natl. Acad. Sci. U.S.A.
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7 Match
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Phaseolus.
1 (sites)
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Pred. No. 4.3e-204;
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Sequence
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Eukaryota;
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Bovidae; Bovinae;
1 (bases 1 to 11)
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Commercial production of chymostin in
Patent: WO 0114571-A 1 01-MAR-2001;
SemBioSys Genetics Inc. (CA)
                                                                                                                                                                                                             (bases 1 to 1173)
          299
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LFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEG
GCQAILDTGTSKLVGPSSDILMYQQAIGATQNQYGEFDIDCINLSYMTTVFEINGKM
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Location/Qualifiers
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Eutheria;
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          agctacatgcctacagttgtcttttgagatcaacggcaagatgtacccactgaccccctcc
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TITLE
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                                            aaatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataa
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Hypoallergenic transgenic soybeans
Patent: WO 01688F-A 2 20-SEP-2001;
E. I. du Pont de Nemours and Company
INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.1%;
nilarity 99.0%;
Conservative
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1. 2970
2. Conganism="synthetic construct"
2. Ab_xref="taxon:32630"
2. Construct"
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Patent WO0168887.
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Pred. No. 5.4e-172;
0; Mismatches 12;
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                                                                                                                           bovine chymosin b (renn 700003 700003 G:162859 chymosin; chymosin B; p bovine (calf) cdna of f Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGTACTATTTGAACTCTCTTACTCTGTATAAAGGTTGGATCATCCTTAAAGTGGGTCT
                                                  Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H., molecular cloning and nucleotide sequence of cdna
chymosin is the major proteolytic enzyme in the unweaned calf. two chromatographically of
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. 1 (bases 1 to 1305)
                       82221400
                                preprochymosin
Nucleic Acids Res. 10,
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(rennin) mrna
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fourth stomach mucosa
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                                (1982)
n the fourth stome different forms,
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                                                  Eaton, M.A.W.,
and Doel, M.T.
a coding for calf
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(see bovchymoa,

enzyme and its precursor are known and a third form see bovchymoa, bovchymoc). this sequence has tentatively

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FEATURES
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                                      ttgatagtcaatactttgggaagatctacctcggaaccccgcctcaagagttcaccgttc
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cagagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagact
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pst-i si
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Location/Qualifiers
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site.
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/db_xref="GI:162860"
/db_xref="GI:162860"
/translation="MRCLVVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
/translation="MRCLVVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFL
QKQOYGISSKYSGFGEVASVPLTUYLLDSQYFGKKIYLGTPFQEFTYLEDFGSSDFWVPS
IYCKSNACKNHQREDPRKSSTFONLGKPLSIHYGTGSMQGILGXDTVTVSUIVDLOQT
YGLSTQEPGDVTYAEEDGILGWAYPSLASEYSLPVFDNMMNRHLVAQDLESVYMDRN
GQESMLTLGALNPSYYTGSLHWYPVTVQQYWQFTVDSYTISGVVVVACEGGCQAILDTG
TSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVVEBINGKMYPLTPSAYT
SQDQGGTCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI"
29...73
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/db_xref="taxon:9913"
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TGAGGAAGCGCTGAAGGAGCATGGGCTTCTGGAGGACTTCCTGCAGAAACAGCAGTATG
         tocgtaaggcgctgaaggaacatggacttctagaagacttcttgcagaaacaacagtatg 1728
                                                                                                                                                                                                                                                                                                                                                                                           ATTCCCAGAAATGGATCCTGGGGGATGTTTTCATCCGAGAGTATTACAGCGTCTTTGACA
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Sequence
AR002347
                                                                                                                                                                               Kato, E.K. and Stuart, W.Dorsey.
Light-regulated promoters for produ
in filamentous fungi
Patent: US 5741665-A 2 21-APR-1998;
                                                                                                                                                                                                                               Unclassified
                                                                                                                                                                                                                                         Unknown
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nilarity 87.4%;
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/db_xref="taxon:32644"
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Mammalia; Eutheria;
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                                 ccttgtctatacactacggtacaggtagcatgcaaggaatcttaggctatgataccgtca
        aagctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaaca
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                                 activity
Patent: E
                                             1 (bases 1 to 1175)
Cashion, L.M., McCaman, M.T.,
Recombinant DNA coding for a
                                                                                               Sequence !
I04058
I04058.1
                                                                           Unknown
                                                                    Unclassified.
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                                                                                                                   I04058
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      Ø
                   EP 0123928-A2 5 07-NOV-1984,
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                    cctccgcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaacc
                                               aagctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaaca
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         agagtactcgatacctgtgtttgacaacatgatgaaccgacacctagtagctcaagactt
                                   tgatagtcaatactttgggaagatctacctcggaaccccgcctcaagagttcaccgttct
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Sequence
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1 (bases 1 to 2726)

1 (bases 1 to 2726)

van den Berg, J.A.D. and Brake, A.J.D.

DNA constructs containing a Kluyveromyces alpha-factor leader sequence for directing secretion of heterologous derivatives Patent: EP 0301669-A1 5 01-FEB-1989;
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coding for bovine carriers. Gene 19, 127-138 (1982) 83054629 (rennin) is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymoc), this sequence has been tentatively identified as chymosin a; it differs from chymosin b by only two amino acids from chymosin c by another amino acid. [1] argues that the
                                                                                                                                                                                                                                                                                                                                                                                                                               ataataactgagctccatctcacttcttctatgaataa
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                                                                                                                                                                       Bovidae; Bovinae; Bos. 1 (bases 1 to 1275)
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chymosin; chymosin A; rennin.
bovine (calf) cdna of fourth stomach
Bos taurus
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/db_xref="taxon:9913"
21. .1166
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195. .1163
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Pred. No. 1.3e-131;
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PRODUCTION OF POLYPEPTIDE
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OS bovine
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PR 17-JUN-1982
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Location/Qualifiers
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pred. No. 1.3e-131;
0; Mismatches 140;
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tccgtaaggcgctgaaggaacatggacttctagaagacttcttgcagaaacaacagtatg
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A15633
A15633.1 GI:491
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1 (bases 1 to 1291)
Carey,N.H., Doel,M.T., Harris,T.J.R.,
A process for the production of a poly
Patent: EP 0068691-A 29 05-JAN-1983;
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nilarity 87.5%;
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Search completed: July 31, 2002, 18:19:33 Job time: 20124 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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897.2	897.4	898.8	1149.8	1173	1226.8	1539	1545.2	3957	Score
22.7	22.7	22.7	29.1	29.6	31.0	38.9	39.0	100.0	Query Match
1175	1240	1291	2970	1173	1244	1547	1558	3957	Query Match Length DB
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AAN40295	AAT03006	AAN91157	AAD17528	AAS00569	AAZ10392	AAX90961	AAZ10376	AAS00570	ID
Sequence encoding	. Chymosin open read	Cloned sequence of	Kunitz soybean try	Bovine pre-pro-chy	Nucleotide sequenc	Phaseolus vulgaris	Nucleotide sequenc	Bovine phaseolin p	Description

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DNA encoding novel Cat pregnancy asso Human stomach cell Human stomach cell Human ovarian tumo Bovine pregnancy a Human aspartyl progastric cancer assopometria melanog Drosophila melanog Drosophila melanog DNA fragment of pa Bovine pregnancy a Bovine pregnancy a	Sequence of recomb Rennin gene. Synt 2.7 Kbp HindIII fr Sequence of prochy Pre-prorennin-A ge BamHI/Sall insert Sequence of prepro cDNA sequence corr Sequence of veal c Sequence of veal c Sequence of proren BamHI insert from Prochymosin (prore Gene encoding (pre Optimised prochymo Human aspartyl pro Prochymosin gene 5 Human stomach cell Human full-length

## ALIGNMENTS

a

RESULT AAS00570 AAS00570 standard; DNA; 3957 BP 14-MAY-2001 AAS00570; \_ (first entry)

Bovine phaseolin promoter pre-pro-chymosin-phaseolin terminator.

Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice; safflower; oil palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant; French bean

Chimeric - Bos sp. Chimeric - Phaseolus vulgaris.

Key Location/Qualifiers

CDS promoter terminator /\*tag= b
/product= "Bovine pre-pro-chymosin"
2727..3957 /noté= "Phaseolin promoter" 1554..2726 /\*tag= 'noté= "Phaseolin terminator /\*tag=

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing chymosin in seeds of transforming plant cell with linked to transcription regul
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Modifying fatty biomass and prod producing acid metabolism in specific n in plants, useful polymers in seeds for increasing

79pp;

is used to construct plasmids for the expression of the p. putida CC faoAB gene. The gene encodes an enzyme that may be used in the CC method of the invention. The specification describes a method for CC manipulating the metabolism of a plant, and comprises expressing a CC heterologous gene encoding fatty acid oxidation enzymes in the CC cytosol or plastids other than the peroxisomes, glyoxisomes or CC mitochondria of the plant. The method may be used to enhance the CC biological production of polyhydroxyalkanoates or novel oil compositions CC in a transgenic plant. Plants which may be used to produce these CC compounds in this way include Brassicas, maize, soybean, cottonseed, cunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco and alfalfa. The method may also be used to production and therefore increase the production of biomass (leaves. CC stems, stalks) by plants. compositions and

Sequence 1244 BP; 456 Ą; 174 c; 178 <u>.</u> 436 Η. 0 other

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                                                                                                                                                                                                                                                                                                                                                                pre-pro-chymosin; rape seed; sunflower; cotton;
barley; oats; sorghum; Arabidopsis thaliana; pot
safflower; oil palm; ground nut; Brazil nut; coc
                                                                                                                                                                                 sig_peptide
  WO200114571-A1
                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chymosin;
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                                                                                                                                                                                                                                                                                                                                                                                                                          transcription regulator; terminator sequence; soybean,
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                                        "Mature bovine
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potato; flax; linseed;
coconut; castor; coriar
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Best Local Similarity
Matches 1173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a DNA which encodes a bovine chymosin polypeptide. Chymosin can be produced in a plant seed through introduction of a chimeric nucleic acid molecule, comprising a nucleic acid sequence encoding a chymosin polypeptide operatively linked to transcription regulator and terminator sequences, into a plant cell. Th sequences are useful for producing plant seeds, in particular seeds of soybean, rape seed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, Arabidopsis thaliana, potato, flax/linseed, safflower, oil palm, groundnut, Brazil nut, coconut, castor, coriander, squash, jojoba and rice.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing chymosin in seeds of plants such as rice, flax, rape seed, transforming plant cell with a nucleic acid encoding chymosin operak linked to transcription regulator and terminator sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing
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                                                     totatacactacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1173; DB 22;
Pred. No. 5.3e-157;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                an; allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1; an vacuolar protein; Gly m 1A; Gly m 1B; rGLY m3; Glychini Gl; b; food; infant formula; animal feed; coating; salad oil; syrup; ing oil; roasting oil; frying oil; cracker; confectionery product; food; topping; sauce; batter; breading mixture; baking mix; dough;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soybean trypsin inhibitor (KSTI) encoding
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cc expression constructs to lower soybean vacuolar protein, commonly known cc as p34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA, CC Gly m IB, rGLY m3 or Glycinin G1 (alaBlb). The allergen content of the expression is reduced by sense suppression which is accomplished by using CC the expression construct that comprises a nucleic acid fragment encoding CC transgenic soybean plants which can be used to make hypoallergenic CC soybean products which can be used to make hypoallergenic CC soybean products which can be used in a variety of food (e.g. infant CC formulas) and animal feed applications. The oil made from seeds of the hypoallergenic transgenic soybean plants can be used as ingredients, CC as coatings, as salad oils, as spraying oils, as roasting oils, and snack foods, confectionery products, syrups and toppings, sauces, CC batter and breading mixtures, baking mixes and doughs. The present CC sequence is a DNA encoding kunitz soybean trypsin inhibitor (KSTI CC cor KTi3), a minor soybean seed allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant expression construct to lower allergen (e.g. Gly content of a soybean, comprises a nucleic acid fragment encocallergen, useful for producing soybean plants which can be useful for producing soybean plants which can be useful for producing soybean plants which can be useful for producing soybean plants.
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2.3e-118;
es 137;
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The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precurso for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospor This can be used to regulate the expression of genes encoding
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        ttcagcaagctattggagccacacagaaccagtacggtgagtttgacatagattgcgaca
                                                                              agttcactgtggacagtgtcaccatcagcggtgtggttgttgtggcctgtgagggtggctgtc
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                     /product= "
/note= "CDS
850..1202
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1203..1442
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1443..2733
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                                                        "oleosin-spacer-Met-prochymosin"
DS contains an intron"
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The DNA which encodes a chimeric fusion protein that consists of the oil-body targeting sequence, a transcription regulation sequence an DNA of the protein of interest can be used to produce antibodies, glycanases, hormones, proteases, protease inhibitors, seed storage proteins, thrombin inhibitors, hirudin, interleukins, chymosin, cys xylanase, carp growth hormone, zein or a collagenase. The enzyme may be cleaved from the oil body protein or used in
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22-FEB-1991;
16-NOV-1993;
30-DEC-1994;
             1929
                                  1870
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                                                                                                                                                                                                                                                                                                                                                association with the oil body fraction.

Allows production of commercially important proteins on a superior to production by conventional systems. The expressed heterologous protein can be easily separated from host cell components due to the use of the oil body as a carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a HindIII fragment containing the oleosin-spacer-Met-prochymosin sequence. This HindIII fragment was joined to a nopaline synthase terminator and cloned into binary vector pCGN1559. The resulting plasmid was called pSBSOTFINT and introduced into A.tumefaciens. The resulting bacterial strain was used to transfole.
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                                                                                         aagatctacctcggaaccccgcctcaagagttcaccgttctctttgatactggttcctct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1669
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Hidaka M;
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                                     ctgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaaccaggtg
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DB; AAP40078.
                 ctgtctccaacattgtggacatccagcagacagtaggcctgagcacccaggagcccgggg
                                                                                            ccctgtctatccactacgggacaggcagcatgcagggcatcctgggctatgacaccgtca
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                                                                                    cagagtactcgatacccgtgtttgacaacatgatgaacaggcacctggtggcccaagacc
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                                          Disclosure;
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AA028632 mi14c08.r
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT BG938320 SOURCE ORGANISM sequence. BG938320 BG938320.1 GI:14337692 EST. BG938320 472 bp mrNA 1Abo15E12 Bovine Abomasum cDNA Library Bos Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos. linear EST 11-JUN-2001 taurus cDNA 5', mRNA

JOURNAL 1 (bases 1 to 472)

Moore, S.S., Hansen, C., Li,C., Fu,A., N

CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Ec

Tel: 780 492 0169
Fax: 780 492 4265 n tissue Meng,Y. and Li,G.

COMMENT

Edmonton, AB,

T6G

2P5, Canada

(rennin) of 0.0

Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA (bovine chymosin a mina) in main database at high score of 928.0 and E-value PCR PRimers

FORWARD: M13 Forward BACKWARD: M13 Reverse

Seq primer: T3 primer
High quality sequence stop:
POLYA=No.

source Location/Qualifiers 472

FEATURES

/organism="Bos taurus"
/db\_xref="taxon:9913"
/clone\_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue\_type="Gastrointestinal tissue (GIT)"
/cell\_type="Epithelial"

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BASE COUNT
ORIGIN
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JOURNAL
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Best Local Similarity
Matches 419; Conserv
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                                                                                                                                                                                                                   Luxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 631)
                          Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project
Contact: Marra M/WashU-NCI Mouse EST Project
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                          Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Pe,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                          PRECURSOR ;, mRNA sequence.
AI892188
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clone is
                mouseest@watson.wustl.edu
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I; Site_2: Xho I"
a 143 c 131 g 94 t
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/lab_host="XL1-BlueMRF'-strain"
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                                                                                            GAGCAAGCCCCTGTTTGTCCAGTATGGTACTGGTAGAATGGAGGGCTTCCTGGCCTACGA
gtactggcaattcactgtggacagtgtcaccatcagcggtgtggtggttgttgcatgtgaagg
                                                     agctattgatccatcctactacacaggatctctttcactgggttccagtcactgtgcagca
                                                                                                                                                   TTTTGCCTCCAAATACTCAGTACCCATATTTGACAACATGATGAACAGGCACCTGGTGGC
                                                                                                                                                                gctcgcgtcagagtactcgatacctgtgttttgacaacatgatgaaccgacacctagtagc 2200
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                                         460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity MGI:293536
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Location/Qualifiers
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73.0%;
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Pred. No. 6.5e-37;
0; Mismatches 170
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POLYA=No.
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CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
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Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3 primer
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The sequence best matches gb:Bo
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/clone_Tib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GI:/cell_type="Epithelial"
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/lab_host="XL1-BlueMRF'-strain"
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89.1%;
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                                                                                                                                                                                                                           Score 354.8; DB Pred. No. 1.9e-36 0; Mismatches 4
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AI326975
AI326975.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mj81e03.x1 Sc
IMAGE:482524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. LC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                      clone was previously sequenced on is from the 3' end
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                                      Eutheria;
1 to 727)
                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:482524"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                           CTGA
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                                                                          sequence.
BG937723
BG937723.1
EST.
                                                                                                                  BG937723
1Abo05D06
                           Bos taurus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
Bovidae; Bovinae; Bos.
 Moore, S.S., cDNA's from
                                                                   COW
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                 (bases 1 to 399)
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nilarity 71.4%;
Conservative
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Hansen, C., Li, C. bovine abomasum
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                                     Cetartiodactyla;
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Pred. No. 2.9e-34;
0; Mismatches 183;
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cDNA Library
  tissue
                                     Craniata; Vertebra
actyla; Ruminantia;
         Fu, A.,
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          Meng, Y.
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minantia; Pecora;
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taurus
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5', mRNA
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Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T3 primer
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
AK004109 1347 bp mRNA linear HTC 19-JAN Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110035E17:PEPSINOGEN F, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
121 c 112 g 77 t
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tissue_type="Gastrointestinal tissue
/cell_type="Epithelial"
/dev_stage="Young adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Bovine Abomasum cDNA Library"
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KS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Butt, C., Adachi, J., Aizawa, K., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Hume, D., Imotani, K., Shiia, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nuazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Sorhimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                                                                                                                                                                                                                                                                                                                 further details.
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caggagagcatgctcacgcttggagctattgatccatcctactacacaggatctcttcac 2297
                                          TGGCTACAAGGCCTCATCCCCCAGAATCTCTTTGCCTTCTACTTGAGCAGCAAGGATGAA
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/db_xref="GI:12835164"
/db_xref="GI:12835164"
/translation="mkmhufldlvalseclvkiplmkiksmrenlresqulkdyleky
rrsrahfulledrrnpaytyepminyldlvyigiisigfppqefrvuldfgssylmyps
rycsspacahhikafnplrssffelvsgrpvnaaygsgemsgflavdfvalglfyvaao,
rglssleepgifmeyavfdgiigicyfpluglgifpypdhlmlogliponlfafylssk
Dekgsmlmlggydpsythgelihydpyskpsymglavdsismnoeviacdggimdf
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/strain="C57BL/6J"
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/dev_stage="18 days embryo"
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                                                         FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence s
                                                                                                                                                                                                                                                                                                                                                    sequence.
BG938086
BG938086.1
EST.
                                                                                                                                                                                                                             Moore, S.S., Hansen, C., Li, C. cDNA's from bovine abomasum Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                  Email: smoore@afns.ualberta.ca
The sequence best matches gb:BPU19786
mRNA, complete cds) in main database a
E-value of 0.0
                                                                                                                                                                                          . Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 AgriFor, Dept of AFNS, U of A,
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/organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                  Mammalia;
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                                                                                                                                                                     (bases
             314 286 1800
314 286 1810
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   mouseest@watson.wustl.edu
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2152 agtactogatacotgtgtttgacaacatgatgaacogacacotagtagotcaagacttgt 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctatcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaacattc
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                                                                                                                                                                                                                                                                                                                                                                                                         mil4c08.rl Soares mouse p3NMf19.5 Mus musculus cDNA IMAGE:463502 5' similar to SW:CHYM_BOVIN P00794 PROC PRECURSORS;, mRNA sequence.
AA028632
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                    Contact: Marra M/Mouse EST Project
                                                                                        Unpublished (1996)
                                                                                                                 The WashU-HHMI Mouse
                                                                                                                                      Waterston, R.
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                AA028632.1 GI:1494769
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I; Site_2: Xho I"
111 c    113 g    76 t
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/sex="Two males and one female mixed"
/tissue_type="gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                                                                                                                                                                                                 Eutheria;
1 to 479)
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88.3%;
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Rodentia;
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Pred. No. 1.8e-29;
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                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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         Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                             ctattgatccatcctactacacaggatctcttcactgggttccagtcactgtgcagcagt 2322
                                                                                                                                                                                                                                                                                                                                                                                                                                      caggtgatgtcttcacctatgcagaattcgatggcatccttggtatggcatacccatcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccgtcactgtctccaacattgtggacattcaacagacagtaggacttagcacccaagaac 2082
                                                                                                                                                                                                                                                                                                                     aagacttgttctcggtttacatggacaggaatggccaggagagcatgctcacgcttggag
                                                                                                                                                                                                                                                                                                                                                                           tcgcgtcagagtactcgatacctgtgttttgacaacatgatgaaccgacacctagtagctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTCACAGTCTCTGATATTGTAGTGTCCCATCAGACTGTGGGCCTGAGTACCCCAGGAAC
                                                                                                                            GCTGCCCTGCCGTTCTGGACACAGGCACTGCGCGCTGTTGACGGGGCCTGGTAGAGACAT 478
                                                                                                                                                                                                                                             CCATCGATCAGTCCTACTTCATAGGCTCACTGCACTGGGTGCCTGTGACAGTACAGGGAT
                                                                                                                                                                                                                                                                                                     AAGACCTGTTCTCCGTTTACATGAGCAGGAATGAGCAGGGGAGCATGCTCACACTGGGGG
                                                                                                                                                                                                                                                                                                                                                              TTGCCTCCAAATACTCAGTACCCATATTTGACAACATGATGAACAGGCACCTGGTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCGACATCTTCACCTACTCTCCATTTGATGGCATCCTGGGCCTGGCCTATCCTACTT 180
                         AI479358 505 bp mRNA linear EST 14-tm27e07.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone mAGE:2157828 3' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
AI479358
             PRECURSOR ;,
                                                       AI479358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

127 c 131 g 117 t
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               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 262; DB 9;
Pred. No. 1.4e-24;
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AUTHORS
TITLE
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Query Match
Best Local Similarity
Matches 303; Conserv
                               2694 aacaacctcgttgggctagctaaagcaatctga 2726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 ACCCTTGNAAGTGTCATCATTGACGGCGTGGTGGTCGTCGTGACGGTGGCTGTCAGGCC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagctattggagccacacagaaccagtacggtgagtttgacatagattgcgacaacctt 2513
                                                                                                                                                                                                                                                                                                                                                     agctacatgcctacagttgtcttttgagatcaacggcaagatgtacccactgaccccctcc
                                                                                                                                  cagaaatggatcttggggagatgtgttcattcgtgagtactacagcgtctttgacagggcc
                                                                                                                                                                                                                                              gcctataccagccaggatcaagggttctgcaccagtggattccagagtgagaaccattcc
AATAACCGTGTGGGGGCTGGCGAAGGCTGTCTGA 113
                                                                                                                                                                                                                  GCCTATACCAGCCAGGACCAGGGCTTTTGCACCAGTGGTTTCCAGGGTGACTATAGTTCC
                                                                                                                                                                                                                                                                                                                           AGCAGCATTCCCACGGCTGTTTTTGAGATCCACGGCAAGAAGTACCCCCTGCCACCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 505)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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1 (bases 1 to 505)
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//lab_host="DHIOB"

//note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with /note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2157828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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77.1%;
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Pred. No. 5.5e-23;
0; Mismatches 90;
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                                                                                                                                                                                                        Matches
                 2363 ggttgttgcatgtgaaggttggatgtcaagctatcttggataccggtacgtccaagctggt 2422
                                                                                   2303 tccagtcactgtgcagcagtactggcaattcactgtggacagtgtcaccatcagcggtgt 2362
                                                                                                                                                      2243 gagcatgctcacgcttggagctattgatccatcctactacacaggatctctttcactgggt 2302
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                                                                 GAGCATGCTCACACTGGGGGCCATCGATCAGTCATACTTCATAGGCTCACTGCACTGGGT 487
AGTGGTGGCTTGTCAAGGTGGCCTGCCCTTCTGGACACAGGCAATGCCCTGTTGAC
                                                                                                                                                                                                          343;
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mi82b01.x1 Soares mouse
mage:473065 3' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:283809
This clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
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AI324867.1 GI:4059296
                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 546)
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                                                                                                                                                                                                                                                                                                           134
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314 286 1810
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:473065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                      6.2%;
                                                                                                                                                                                                      Score 246; DB 9;
Pred. No. 1.5e-22;
0; Mismatches 135
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                                                                                                                                                                                                      Mismatches 135;
                                                                                                                                                                                                                                    Length 546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caccagtggattccagagtgagaaccattcccagaaatggatcttgggagatgtgttcat
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI385490 517 bp mRNA linear EST 27-JAN-1999 mj81e03.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE: 82524 5' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
                                                                                                                                                                                                             High
                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                       Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                               Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                Possible reversed clone: similarity
                                                                                                                                                                                                                                                                    correct orientation)
                                                                                                                                                                                                                                                                                     This read is a RESEQUENCE of a previously This read has been verified (found to hit
                                                                                                                                                                                                                                                                                                                         MGI:293268
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                                                                                                                                                                                       quality sequence stop: 442
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   314 286 1800
314 286 1810
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st st
was primed with a Not I - oligo(dT) primer [5'
                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:482524"
                                                                                             /clone_lib="Soares mouse p3NMF19.5"
                                                                                                                                                    /organism="Mus musculus"
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1 to 517)
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Rodentia;
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                                                                                                                                                                                                                                                  wrong strand
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                                                                                                                                                                                                                                                                                     sequenced mouse clone its original self in
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   1st strand cDNA [5'
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REFERENCE
AUTHORS
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcaacagacagtaggacttagcacccaagaacc
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                                                                               Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                   Carninci, P.,
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                               AKOO8959 mRNA linear HTC 19-JAN-2002 MUS musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416016:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
                                                                                                                                                                                                  clone:2210416016.
                                                                                                                                                                                                                                               HTC; CAP trapper.
                                                                                                                                                                                                                                                                    AK008959.1 GI:12843460
 Itoh, M., Konno, H.,
                                                                                                                                   (sites)
                                    (sites)
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70.9%;
                                                                                                                                                 Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2083
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EE 5 (bases 1 to 1385)

EB 6 (bases 1 to 1385)

EB 7 (bases 1 to 1385)

RRS Adachi, J., Alazawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, T., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction Rot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        = 25.0. Second sequence [5'
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20499374
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                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1895643"
/db_xref="taxon:10090"
/tissue_type="stomach"
/clone_lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                             /clone="2210416016"
                                                                                                                                                               /sex="male"
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                                                                                         ACCACCGCCTTGCAGGGCATGTTGGGGGGAGGGCGCTCTGTCCCAGCCCCTCTTCGGTGTC
                                                                                                                                                                                                                                                                                       cactacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaac
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tcctactacacaggatctcttcactgggttccagtcactgtgcagcagtactggcaattc
                               TACCTTGGCAGCCAGCAGGGTCTAACGGCGGGCAGATTGTGTTCGGTGGCGTGGACGAG
                                                      tacatggacaggaatggccaggaggat-----gctcacgcttggagctattgatcca
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                                                                                                                                                                                                              ATCCAGGTCCCTAACCAGGAGTTCGGCCTGAGTGAGAATGAGCCTGGCACCAATTTTGTC
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                                                                                                                                                                                                                                                                        CAGTACGGCACCGGCAGCCTTACCGGCTTCTTCGGCTATGACACTCTGAGAGTCCAAAGC
                                                                                                                                                                                                                                                                                                                                   ACCCGCTACAACCCCAGCAAGTCCTCCACCTACTACACTCAAGGGCAGACCTTCTCCCTG
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/protein_id="Bab25990.1"
/db_xref="GI:12843461"
/translation="mkmmyvallclplleaalirvplkkmksiretmkeogvlkdflk
/translation="mkmmyvallclplleaalirvplkkmksiretmkeogvlkdflk
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ssyycoseactthtrynpsksstyytogotfsloygflgsltgfffgydtlrvosiovpn
oefglsenefgtnfyxaofdolmglaypglssgattalogmlgealsoplegvylg
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1385
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GIVDTGTSLLVMPAQYLNELLQTIGAQEGEYGQYFVSCDSVSSLPTLTFVLNGVQFPL
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441 c 336
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53.7%;
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Pred. No. 1.9e-21;
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1131 CTGAACGCTGAGAGTGGCCAGCCCCTCTGGATCCTCGGGGGATGTCTTCCTCAGGTCTTAC
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl~&t2=MR1-SN0064-150
500-004-a03&t3=2000-05-15&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 619)
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MR1-SN0064-150500-004-a03
                                                                    High quality sequence start: 10
High quality sequence stop: 619
Location/Qualifiers
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                                                                                                                                                       Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
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                                                       1. .619
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atacccatcgctcgcgtcagagtactcgatacctgtgttttgacaacatgatgaaccgaca
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                                                                                                                                                                                                                        AK008886 1388 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210410106:homolog to GASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C), full insert sequence.
                                            Mus musculus
                          Eukaryota; Metazoa;
                                                                           clone: 2210410L06.
                                                                                                   Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
                                                                                                                                                                           AK008886.1 GI:12843349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
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  Eutheria;
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Chordata;
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Pred. No. 2.8e-21;
0; Mismatches 215
Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                                                                   male stomach cDNA mouse cDNA library
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  Muridae; Murinae; Mus
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                          Euteleostomi;
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  source
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E 5 (bases 1 to 1388)

E Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hori, F., Hiraka, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fijiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Direct Submission

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                            Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   URL:http://genome.gsc.riken.go.jp/, Fax:81-45-503-9216)
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Hayashizaki,Y.
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                                                                                                                          sequence
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                       GCAGCTTTGATCAGGGTCCCCCCGAAGAAAATGAAGAGTATCCGGGAGACCATGAAGGAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gctgagatcacccgcattcctctctacaaaggtaagtctctccgtaaggcgctgaaggaa 1688
                                                                                                               attgtggacattcaacagacagtaggacttagcacccaagaaccaggtgatgtcttcacc
                                                                                                                                                                               CAGTACGGCACCGGCAGCCTTACCGGCTTCTTCGGCTATGACACTCTGAGAGTCCAAAGC
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                                                                                                                                                                                                                                                                           ACCCGCTACAACCCCAGCAAGTCCTCCACCTACTACACTCAAGGGCAGACCTTCTCCCTG
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TACGCCCAATTTGACGGGATCATGGGCCTGGCCTACCCCGGCCTGTCTTCAGGGGGGCGCC
                                                                                          ATCCAGGTCCCTAACCAGGAGTTCGGCCTGAGTGAGAATGAGCCTGGCACCAATTTTGTC
                                                                                                                                                                                                                                                                                                                                                                     GGCTCCTCCAACCTGTGGGTGTCTTCTGTCTACTGCCAGAGCGAGGCCTGCACCACACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGGCAAGTTTGGTGACTACAGTGTACTCTATGAGCCCATGGCCTATATGGATGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcttcggtgaagttgctagcgtgccacttaccaa-----ctaccttgatagtcaa 1799
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/protein_id="BAB25952.1"
/db_xref="G1:12843350"
/db_xref="G1:12843350"
/translation="MKMMVVALLCLPLLEAALIRVPPKKMKSIRETMKEQGVLKDFLK
/translation="MKMMVVALLCLPLLEAALIRVPPKKMKSIRETMKEQGVLKDFLK
VHKYDPGQKYLHFGKFGQVSULYEPMAYMDASYYGEISIGTPPQNFLTURQTGSIQVPN
QEFGLSENEPGTNFVYAQFDGTMGLAYPGLSGGAFTALQGMLGEGALSQPLEGVYLG
SQGGSNGGQIVFGGVDENLYTGELTMIPVTQBLYQGITDLGNQASGGCSSGCQ
GIVDTGTSLLVMPAQYLMELLQTIGAQDGEYGQYFVSCDSVSSLPTLTFVLNGVQFPL
SPSSYIIQEEGSCMVGLESLSLNAESGQPLWILGDVFLRSYYASSTWAITGWALPLLS
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1895666"
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/clone_lib="RIKEN full-length enriched
/dev_stage="adult"
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SOURCE
ORGANISM
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Districh, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                    correct orientation)
Putative full length read
                                                                                                                           This read is a RESEQUENCE of
This read has been verified
                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R
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                                                   primer: -40RP from Gibco
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314 286 1810
                              quality sequence stop: 395
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               Location/Qualifiers
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ACATCGACTGCTGGAGGCTGGACATCATGCCCACCGTTGTCTTTGAGATCCATG 414
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is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
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4: /cgn2_6/ptodata/2,
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US-08-318-193-15

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US-09-080-718-16

US-09-080-718-16

US-09-080-718-16

US-08-631-097-7

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        Sequence 2, Appli Sequence 1, Appli Sequence 15, Appl Patent No. 5210327 Patent No. 5200327 Patent No. 5200327 Sequence 4, Appli Sequence 4, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli
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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.9	1.9	1.9	1.9	1.9	1.9	1.9
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	ω	Sequence 13, Appl	Sequence 1, Appli	1,	Sequence 1, Appli	Sequence 186, App	Patent No. 5231168	Sequence 32, Appl		Sequence 32, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 15, Appl	Sequence 11, Appl	Sequence 13, Appl

## ALIGNMENTS

RESULT 1 US-08-240-372-2

Sequence 2, Application US/08240372 Patent No. 5741665

GENERAL INFORMATION:
APPLICANT: KATO, ELIE K.
APPLICANT: STUART, W. DORSEY
APPLICANT: STUART, W. DORSEY
TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGINUMBER OF SEQUENCES: 2

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Qy
                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
US-08-240-372-2
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE, DOCKET NUMBER: 3918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                          Query Match
Best Local Sin
Matches 982;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,372
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1609 tcgttgctgttactcacgctgctgagatcaccccgcattcctctacaaaaggtaagtctc 1668
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CITY: Washington,
COUNTRY: USA
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US-08-846-021A-6
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Matches 972;
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/846,021A
FILING DATE: APRIL 25, 1997
CLASSIFICATION: 800
CLASSIFICATION: 800
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
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LOCATION:
FEATURE:
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 93:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: BERESKIN & PARR
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72; Conservative
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M5H 3Y2
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(416) 361-1398
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Preparation of Heterologous
Oil Bodies
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Pred. No. 3.5e-175;
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RESULT 3
5217891-14
; Patent No. 5217891
; APPLICANT: BRAKE, ANT
; TITLE OF INVENTION: D
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                                  NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 09-APR-1990
PRIOR APPLICATION DATA:
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                     APPLICATION NUMBER: FILING DATE: 28-JUL
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US-08-318-193-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE: US 07/
APPLICATION NUMBER: US 07/
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                              KEGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEFAX: (703)63-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2749
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APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GARVIN, Robert T. APPLICANT: MALEK, Lawrence T.
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                                                                                                   FEATURE
                                                                                                                               MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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TELEFAX: 899149
                              NAME/KEY:
LOCATION:
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CITY: Alexandria
STATE: Virginia
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Synthetic DNA
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OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
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5200327-6
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5200327-6
;PATENT NO. 5200327
; PATENT NO. 5200327
; APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
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CURRENT APPLICATION DATA:
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         caagaaccaccaaagattcgatccgagaaag 1940
                                                              tatctcctccaagtactctggtttcggtgaagtcgcttccgttccattgaccaactactt
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Pred. No. 3.9e-33;
0; Mismatches 80
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETIC;
BIOACTIVE HUMAN GRANULCCYTE MACROPHAGE COLONY STHMULATING
; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREPTOMYCES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             APPLICANT: GARVIN, ROBERT T.
APPLICANT: MALEK, LAWYENCE T.
TITLE OF INVENTION: AN EXPREST
TITLE OF INVENTION: OF BIOACTITITLE OF INVENTION: STIMULATING
TITLE OF INVENTION: PROTEINS F.
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1687
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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CITY: Alexandria
STATE: Virginia
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 APPLICATION NUMBER:
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                               22313-0299
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                                                                                                                                                                                                      1800 Diagonal Road,
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                                                                                                                                                                                                                         Foley & Lardner
                                                                                                                                                                                                                                                                         AN EXPRESSION SYSTEM FOR THE SECRETION
OF BIOACTIVE HUMAN GRANULCCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM.-CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOMYCES
US/08/318,193
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                                                                                                                                                                                                      Suite 500
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                                      Version
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                                                                                                                                          Sequence 6, Application Patent No. 6232454
GENERAL INFORMATION:
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Best Local Similarity
Matches 245; Conserv
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SEQUENCE CHARACTERISTICS:
                                       APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                               1927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: dou
TOPOLOGY: linear
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76.3%;
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Pred. No. 2.1e-32;
0; Mismatches 76;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                     2054
                                                                                                                                                 1994 tagcatgcaaggaatcttaggctatgataccgtcactgtctccaacattgtggacattca 2053
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: PANCT
CLONE: 1515165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agaagacttcttgcagaaacaacagtatggcatca----gcagcaagtactccggctt 1753
                                                                                                                                                                                                                                                                                                                                           ctacctcggaaccccgctcaagagttcaccgttctctttgatactggttcctctgactt 1873
                                                                                                                                                                                                                                                                                                                                                                                                                cggtgaagttgctagcgtgccacttaccaactaccttgatagtcaatactttgggaagat 1813
                                                                          acagacagtaggacttagcacccaagaaccaggtgatgtcttcacctatgcagaattcga
                                                                                                                                                                                                           gagaaagtegteeacetteeagaaettaggeaaaecettgtetataeaetaeggtaeagg 1993
tggcatccttggtatggcatacccatcgctcgcgtcagagtactcgatacctgtgttttga
                                                   CCAGCAGTTTGGAGAAAGTGTCACAGAGCCAGGCCAGACCTTTGTGGATGCAGAGTTTGA
                                                                                                                        GAGCTTGTCCGGGATCATTGGAGCCGACCAAGTCTCTGTGGAAGGACTAACCGTGGTTGG
                                                                                                                                                                                      TTCCCAGTCCAGCACATACAGCCAGCCAGGTCAATCTTTCTCCATTCAGTATGGAACCGG
                                                                                                                                                                                                                                                         CTGGGTCCCCTCTGTGTACTGCACTAGCCCAGCCTGCAAGACGCACAGCAGGTTCCAGCC
                                                                                                                                                                                                                                                                                                                             CTCCATTGGCTCCCCACCACAGAACTTCACTGTCATCTTCGACACTGGCTCCTCCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                GGACCAGAGTGCCAAGGAACCCCTCATCAACTACTTGGATATGGAATACTTCGGCACTAT
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US-08-723-938-4
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                                                                     CLONE:
US-08-723-938-4
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Query Match
Best Local Similarity
Matches 421; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, APPLICANT: Coleman,
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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                                                                                                            IMMEDIATE SOURCE:
                                                                         MMEULL: LULL LIBRARY: LULL 11BRARY: 312099
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                         LENGTH:
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  Conservative
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TWO NOVEL HUMAN CATHESPIN PROTEINS
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US-09-080-538-4
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                                                                                                                                                                                                                Sequence 4, Application US/09080538 Patent No. 5965129
                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
TITLE OF INVENTION: TWO NOVEL
COMPUTER READABLE FORM:
                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                             CORRESPONDENCE ADDRESS:
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               COUNTRY: UZIP: 94304
                                                              STREET: 3174 Po:
CITY: Palo Alto
                                                STATE:
                                                                              ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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                                                                                                                                                HUMAN CATHESPIN PROTEINS
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Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 1299 base pair
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LIBRARY: LUNGN
CLONE: 312099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
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REGISTRATION NUMBER:
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COMPUTER: IB
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                                         GGAGCAGGGGCTATTGGATAAGCCTGTCTTCTCCTTTTACCTCAACAGGGACCCTGAAGA
                                                                         gaaccgacacctagtagctcaagacttgttctcggtttacatggacaggaatggccagga 2242
                                                                                                                                                    tggtatggcatacccatcgctcgcgtcagagtactcgatacctgtgttttgacaacatgat 2182
                                                                                                                                                                                            CGGGGAGGCTCTCTGGGAGCCCAGCCTGGTCTTCGCCTTTTGCCCCATTTTGATGGGATATT 576
                                                                                                                   TGGAATCCTGAGCGAGGACAAGCTGACTATTGGTGGAATCAAGGGTGCATCAGTGATTTT 516
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Pred. No. 1.7e-21;
0; Mismatches 399;
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US-08-974-691-7
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                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 166
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                               TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2294
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                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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STREET: St.
CITY: Atlan
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paint
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60 FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Atlanta
STATE: GA
                                   TOPOLOGY:
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 30309-3450
                                              STRANDEDNESS: single
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                                                                              ENGTH:
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                                   linear
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US-09-008-271A-16

Sequence 16, Application Patent No. 6203979
GENERAL INFORMATION:

6, Application 6203979

US/09008271A

APPLICANT:

Bandman, Hillman,

Olga Jennifer

RESULT

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; ORIGINAL SOURCE:
; ORGANISM: HOM
US-08-974-691-7
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                        CTTGCTGGCTGGGGAGTACATCATCCTGTGCTCGGAAATCCCAAAGCTCCCCGCAGTCTC
                                                                      gaaccagtacggtgagtttgacatagattgcgacaaccttagctacatgcctacagttgt
                                                                                                                                                         GGGCCCAGGGCTGACTCTCTGTGCCAAGGGCTGTGCTGCCATCCTGGATACGGGCACGTC
                                                                                                                                                                                                                                   tcactgggttccagtcactgtgcagcagtactggcaattcactgtggacagtgtcaccat
                                                                                                                                                                                                                                                                                                                                                                      TGGAATCCTGAGCGAGGACAAGCTGACTATTGGTGGAATCAAGGGTGCATCAGTGATTTT
CTTCCTTCGGGGGGGTCTGGTTTAACCTCACGGCCCATGATTACGTCATCCAG
                                                                                                                      caagctggtcggacctagcagcgacattctcaacattcagcaagctattggagccacaca
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                                                                                                       Similarity
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Pred. No. 1.9e-21;
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US-09-008-271A-16
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                 1091
                                                                                                                                                                1943
                                                                                                                                                                                                                                                                                                                                                     1769 cgtgccacttaccaactaccttgatagtcaatactttgggaagatctacctcggaacccc 1828
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                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CGGGGAGGCTCTCTGGGAGCCCAGCCTGGTCTTCGCCTTTTTGCCCATTTTTGATGGGATATT
               aggacttagcacccaagaaccaggtgatgtcttcacctatgcagaattcgatggcatcct
                                                                                                                             TAGCTCCTTCCAGGCCAATGGGACCAAGTTTGCCATTCAATATGGAACTGGGCGGGTAGA
                                                                                                                                               gtccaccttccagaacttaggcaaacccttgtctatacactacggtacaggtagcatgca
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                                                                                            GAGATGCCACTTCTTCAGTGTGCCCTGCTGGTTACACCACCGATTTGATCCCAAAGCCTC
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                                                              TGGAATCCTGAGCGAGGACAAGCTGACTATTGGTGGAATCAAGGGTGCATCAGTGATTTT
                                                                                                                                                                                                                                                                  TCCACAAAACTTCACTGTTGCCTTTGACACTGGCTCCTCCAATCTCTGGGTCCCGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
CLONE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: SEQ
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Shah, Purvi
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Corley, Neil C.
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APPLICANT: KINChL, A
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08631097 Patent No. 5968816
                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: YOU CITY: Washington STATE: D.C.
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                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11598
FILING DATE: 12-Oct-94
ATTORNEY/AGENT INFORMATION:
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                                                                                         TELEPHONE: (202)463-7700
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                       NAME: Cohen, Herbert REGISTRATION NUMBER: 25,109 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                       FILING DATE: 12
CLASSIFICATION:
STRANDEDNESS
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                         LENGTH:
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Tumor Suppressor Genes,
Proten Encloded Thereby, and Use of Said Genes and Protein
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Linear

Genomic

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; LOCATION: not available; iDENTIFICATION METHOD: experiment-IDENTIFICATION METHOD: in specification; OTHER INFORMATION: prevention of IFN-2; OTHER INFORMATION: provided cell death; PUBLICATION INFORMATION: not available US-08-631-097-7
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Best Local S
Matches 443
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ORIGINAL SOURCE:
ORGANISM: homo sa
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
UNITS: not applicable
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CLONE: no
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LOCATION:
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CELL LINE:
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                                                                     CAACAACGTGCTGCCCGTCTTCGACAACCTGATGCAGCAGAAGCTGGTGGACCAGAACAT
                                                                                                                                          CACCTTCATCGCAGCCAAGTTCGATGGCATCCTGGGCATGGCCTACCCCCGCATCTCCGT
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CTTCTCCTTCTACCTGAGCAGGGACCCAGATGCGCAGCCTGGGGGGTGAGCTGATGCTGGG
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Pred. No. 1e-19
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 11
; LENGTH: 2038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-810-712-11
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Patent No. 6160106
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins
TITLE OF INVENTION: Use of said Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 443; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: sequencelist CURRENT APPLICATION NUMBER: US/08/810,712G CURRENT FILING DATE: 1997-03-03
EARLIER APPLICATION NUMBER: PCT/US94/11598
EARLIER FILING DATE: 1994-10-12
NUMBER OF SEQ. ID NOS: 31
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Pred. No. 1e-19;
0; Mismatches 378;
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APPLICANT: Tang, J. N.
                                                                      FILING DATE: 19920922
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
            TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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SEQUENCE
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STATE: Georgia
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; FEATURE:
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; LOCATION: 2460..2465
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## ALIGNMENTS

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SOURCE
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DEFINITION
ACCESSION RESULT AX088019 FEATURES REFERENCE AUTHORS TITLE JOURNAL source 1 (bases 1 to 1173)
van Rooijen,G., Keon,R.G., Boothe,J. and Shen,Y. Commercial production of chymosin in plants Patent: WO 0114571-A 1 01-MAR-2001; SemBioSys Genetics Inc. (CA)
Location/Qualifiers AX088019 1173 bp Sequence 1 from Patent WO0114571. AX088019 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bos taurus Bovidae; Bovinae; Bos. AX088019.1 GI:13396947 /organism="Bos taurus" /db\_xref="taxon:9913" 1. .1173 /note="unnamed protein product" 1. .1173 DNA linear PAT 17-MAR-2001

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SNIVDIQQTVGLSTQEPGDVETYAEFDGILGMAYPSLASEYSIFVFDNMMNRHLVAQD
LFSVYMDRNQQESMLTLGAIDPSYYTGSLHWVPVTVQQYMQFTVDSVTISGVVVACEG
GCQAILDTGYSKLVQPSSDILNQATGATQNQYGEFDLDCDNLSYMTTVVFEINGM
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van Rooijen,G., Keon,R.G., Boothe,J. and Shvan Rooijen,G., Roon,R.G., Boothe,J. and Shvan Rooijen,G., Rooijen,G., Rooijen,G., Boothe,J. and Shvan Rooijen,G., Ro
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        aacaacctcgttgggctagctaaagcaatctga
                                                                actgtggacagtgtcaccatcagcggtgttgttgcatgtgaaggtggatgtcaagct
                                                                                                                                                                                                                                                                                                          agcagcaagtactccggcttcggtgaagttgctagcgtgccacttaccaactaccttgat
AACAACCTCGTTGGGCTAGCTAAAGCAATCTGA
                                         cagaaatggatcttggggagatgtgttcattcgtgagtactacagcgtctttgacagggcc
                                                                                                                                                                             atcttggataccggtacgtccaagctggtcggacctagcagcgacattctcaacattcag
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Bovine chymosin C (renni J00004
J00004
J00004 I GI:162861
chymosin; chymosin C; pr
Bos taurus calf fourth s
Bos taurus
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CDNA sequence encod
E00079
E00079.1 GI:216838
JP 1983032896-A/1.
unidentified.
unidentified
1 (bases
Beppu,T.,
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82189915
                                                                                                                                                                                                                                                                         ch 4.8%;
l Similarity 100.0%
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence implies that this sequence might be a pseudogene mrna, or there may be an error in the cona. the amino acid sequence deduced from this nucleotide sequence differs at three sites from bovine chymosin a (see bovchymoa) and at four sites from bovine chymosin is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the unweaned calf. two chromatographically different forms, a are b, of the enzyme and its precursor are known and a third form, represented by this sequence, seems likely. the presence of a termination codon (bases 27-29) within the prepropeptide coding
                               unclassified
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1 (bases 1 to 12
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
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/db_xref="taxon:9913"
/tissue_type="fourth stomach mucosa"
/dev_stage="calf"
<1. 1269
                                                                                                                                                                                                                                                                                                                                                                 /translation="MQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGM AYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWV PVTVQQYMQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQN QYDEFDIDCDMLSYMPTVVFEINGKIYPLTPSAYTGQDQGFCTTGFQSENHSQKWILG DVFIREYYSVFDRANNLVGLAKTI"

3 81 c 321 g 268 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="chymosin C"
/protein_id="AAA30449.1"
/db_xref="GI:457097"
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                 t to
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 Uozumi,T.
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JOURNAL
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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PATENT: JP 1983032896-A 1 25-FEB-1983;
BEPPU TERUHIKO
OS calf
PN JP 1983032896-A/1
PN JP 1983032896-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u
                                                                                                      patent: JP 1990109984-A 1 23
BEPPU TERUHIKO
OS BOVİNE
PN JP 1990109984-A/1
PD 23-APR-1990
PF 01-DEC-1988 JP 19883021
PI BEPPU TERUHIKO, UOZUMI
C12N15/59,C12N1/21;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=St
FH Key Locatic
FH Key 1.109
FT CDS /produc
FT CDS /produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beppu, T., Uozumi, T. and Nishimori, K. .
COMPLEX PLASMID AND MICROORGANISM CONTAINING
Patent: JP 1990109984-A 1 23-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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    252
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01-DEC-1988 JP 1988302176
BEPPU TERRHIKO, UOZUMI TAKESHI, NISHIMORI KATSUHIKO
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Location/Qualifiers
1. 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
                                                     /product='
Location/Qualifiers
1. .1098
/db_xref="taxon:9913"
327 c 300 g
                                            /organism="Bos taurus"
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Best Local
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Best Local Similarity
Matches 49; Conserv
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49; Conserv
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        Wosnick, M.A.,
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581 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 629
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                                                                                                   SYNPROCAA
Synthetic bovine proc
M22593 M18758
M22593.1 GI:209139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-AUG-1999) Molecular Biology Unit, Animal Biotechnology Centre, National Dairy Research Institute, Karnal, Haryana 132001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chorda:
Mammalia; Eutheria; Cetart:
Bovidae; Bovinae; Bubalus.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Batish, V.K., Mukhopadhyay, U.K., Mohanty, A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bubalus bubalis
            synthetic construct artificial sequence.
1 (bases 1 to 1115)
                                                                prochymosin.
Synthetic DNA.
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                                                                                                                                                                                                                                                                                                             4.2%; ilarity 100.0%; Conservative
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EVASVPLTNYLDSQYFGKIYLGTPPQEETVLFDTGSSDFWVPSIYCKSNACKHIQFFD
PRKSSTFQNLGKPLSIRYGTGSMOGILGYDTATVSNIVDLOQTVGLSTQBEDFUPADA
EFDGILGMAYPSLASEYSIPVFDNMMNHHLVAODLFSVYMDRNGQESMLTLGALDPSY
YTGSLHWVPUTYQQYWQFTVDSITISGYVVVACEGGCQALLDTGTSKLVGPSSDILNIQ
QAIGATQNQYGEFDIDCDNLSYMPTVVSEINGKMYPLTPSAYTSQDQGFCTSGFQSEN
RSQOWILGDVFIREYXYSVFDRANNLVGLAKAI"

336 c 306 g 215 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="prochymosin"
/protein_id="AAF27315.1"
/db_xref="GI:6739580"
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100.0%;
Barnett, R.W.,
                                                                                                                                     prochymosin
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Pred. No.
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 Vicentini, A.M.,
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7.5e-15;
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   Erfle, H.,
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   Elliott, R.,
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4.2%; Score 49; DB
Best Local Similarity 100.0%; Pred. No. 7.
Matches 49; Conservative 0; Mismatches
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                                                                                                                                                                                                               AR002347
Sequence 2 from patent
AR002347
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Cashion, L.M., McCaman, M.T., Rice, C.W. and Sias, S.R.
Recombinant DNA coding for a polypeptide displaying
                                        Light-regulated promoters for production in filamentous fingi Patent: US 5741665-A 2 21-APR-1998; Location/Qualifiers 1. 1240
                                                                                                             1 (bases 1 to 1240)
Kato, E.K. and Stuart, W. Dorsey.
                                                                                                                                                        Unknown
                                                                                                                                                                                                  AR002347.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rapid construction of large synthetic genes: total chemical synthesis of two different versions of the bovine prochymosin Gene 60, 115-127 (1987)
                                                                                                                                         Unclassified.
                                                                                                                                                                       Unknown.
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downstream of HindIII site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP 0123928-A2 5 07-NOV-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
356 c 318 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1175
             ∕organism="unknown"
374 c 339 g
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1. .1115
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US 5741665
              253
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7.4e-15;
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                                                                                              of heterologous proteins
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                                                                                              Local Similarity 100.0%; In the second secon
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11
                                                                                                                                                                                                                                                                                                                                                                                                          /product="chymosin a"
293 a 391 c 336 g
20 bases upstream from codon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymosin (rennin) is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically distinct forms are known and a third seems likely (see bovchymob and bovchymoc). this sequence has been tentatively identified as chymosin a; it differs from chymosin b by only two amino acids and from chymosin c by another amino acid. [1] argues that the different chymosins are probably polymorphic variants of a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 19, 127-138 (1982)
83054629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chymosin; chymosin A; rennin.
bovine (calf) cdna of fourth stomach mucosa mrna.
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Taunton-Rigby,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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QKQQYGISSKYSGFGEVASVPLINYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPS
IYCKSNACKNHQFFDFGKSYFQLLGKPLSIHYGTGSNGGILGYDTWTVSNILDIQQT
VGLSTQEPGGTFYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFGIVDRN
GQESMLTLGALDPCYYTGSLHWPVTYQQYMQFTVDSVTISGYVVACEGGCQAILDTG
TSKLVGPSSDILNIQQAIGATQNQYDEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYT
SQDQQFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLYGLAKAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="presequence"
195. .1163
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/protein_id="AAA30447.1"
/db_xref="GI:162858"
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100.0%; Pred. No. 7.3
1ve 0; Mismatches
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a (rennin) mrna
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3. 7.3e-15;
0;
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RESULT E00144

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OS bovine calf
PN JP 1984021392-A/1
PD 03-FEB-1984
PF 30-JUN-1983 JP 1983119481
PR 01-JUL-1982 US 82 394433, 13-APR-1983 US 83 484539 PI
CHYYAARUSU EI BASURETSUTO
PC C12N15/00,C07H21/04,C12N1/20,C12P19/34,C12P21/02,(C12N15/00, PC C12N1:19);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC manti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC manti-sense: No;
CC anti-sense: No;
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A15836
A15836.1 GI:48
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cDNA e1
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                                                                                                                           heterologous proteins
Patent: EP 0307011-A 5 15-MAR-1989;
NEDERLANDS INSTITUT VOOR ZUIVELOND
                                                                                                                                                                                                              DNA fragments, containing a lactic acid bacterium-specific regulator region for the expression of genes coding for no
                                                                                                                                                                                                                                                         1 (bases 1 to 1291)
Simons, A.F.M. and De Vos, W.M.
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Location/Qualifiers
1. 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
388 c 329 g 26
/db_xref="taxon:9913"
382 c 328 g
                                                                                                     Location/Qualifiers
                                                     organism="Bos taurus"
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7.3e-15;
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 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGGAGCATGCTCACGCT
                                                                     l Similarity
49; Conserv
                                                                                                                                                            pst-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chymosin is the major proteolytic enzyme in the fourth stomach of the unweaned calf. two chromatographically different forms, a and b, of the enzyme and its precursor are known and a third form see likely (see bovchymoa, bovchymoc). this sequence has tentatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris,T.J.R., Lowe,P.A., Lyons,A., Thomas,P.G., Eaton,M.A.W., Millican,T.A., Patel,T.P., Bose,C.C., Carey,N.H. and Doel,M.T. molecular cloning and nucleotide sequence of cdna coding for calf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine chymosin b (rennin) J00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    been identified as coding for preprochymosin b. sequence comparison indicates that the precursors for chymosins a and b differ by only two amino acids, and for b and c by only four amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82221400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 10, 2177-2187 (1982)
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bovine (calf) cdna
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larity 100.0%; F
Conservative 0;
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/db_xref="taxon:9913"
<1. .1305</pre>
                                                                                                                                                                                                                                                                                   VGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRN
GQESMLTLGAINPSYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="chymob mRNA"
26. .1171
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393 c 340 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="preprochymosin b"
                                                                                                                                                                                                                              note="presequence"
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RESULT 15
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Best Local Similarity 100.0%; I
Matches 49; Conservative 0;
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                            source
                                                                                                     656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                            833 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 881
                                                                                                                                                                                                                      1460 bp cDNA encoding pre-prorennin A. E00295 E00295.1 GI:2168583 JP 1985058077-A/3.
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1460 bp

DNA coding of pre-pro rennin.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jierarudo, F.B.
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440 c 398 g
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833 TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 881
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Bovidae; Bovinae;
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                               Conservative
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                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
437 c 400 g
                                      100.0%;
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                                      Score 49;
Pred. No.
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Search completed: August Job time: 16797 sec 1, 2002, 01:41:47

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Database :
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AAT03006 AAN40055	AAQ20949 AAQ14051	AAQ04683 AAN40295	AAN30063	AAS00570	AAS00569	ID
Chymosin open read Sequence of prochy	Prochymosin (prore Rennin gene. Synt	Sequence encoding Sequence encoding	Sequence of proren	Bovine phaseolin p	Bovine pre-pro-chy	Description

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## ALIGNMENTS

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AASOO569
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                                                                                                                                                                Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thaliana; potato; flax; linseed; rice safflower; oll palm; ground nut; Brazil nut; coconut; castor; coriander; squash; jojoba; ds.
                                                                                     sig_peptide
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WO200114571-A1.
                                     mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing chymosin in seeds of plants such as rice, flax, rape transforming plant cell with a nucleic acid encoding chymosin linked to transcription regulator and terminator sequences - \frac{1}{2}
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DB; AAU00536.
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                                                                                                             gatactggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaag
                                                                                                                      gatactggttcctctgacttctgggttccctctatctactgcaagagcaatgcctgcaag
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                                      tctatacactacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtc
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                      "Bovine
                                                                                                                                                                                                                                                                                                                             lator; terminator sequence; soybean; (sunflower; cotton; tobacco; alfalfa;
                      pre-pro-chymosin"
                                                                                       promoter'
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linseed; rice
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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tctatacactacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtc
                                                                   aaccaccaaagattcgatccgagaaagtcgtccaccttccagaacttaggcaaacccttg
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aacaacctcgttgggctagctaaagcaatctga
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Location/Qualifiers
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Matches 49
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim recombinant plasmids contg. the cDNA of prorennin. Specified plasmids are pCR 10001 and pCR2001 (cc whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coli C 391710) contg. plasmid pCR2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid contg. calf microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1981;
                                               Protein
plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 20-23; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beppu T,
                                                                                                                                                                                                                                                              05-OCT-1990
                                                                                                                                                                                                                                                                                             AAQ04683 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BEPP/) BEPPU
                                                                                       Complex plasmid and microbe - contains
                                                                                                        P-PSDB; AAR05080.
                                                                                                                                               01-JAN-1988;
                                                                                                                                                                01-JAN-1988;
                                                                                                                                                                                               JP02109984-A
                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                             Pro-rennin;
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                                 Sequence 1098
                                                                        Disclosure;
                                                                                                                WPI; 1990-168358/22.
                                                                                                                               (BEPP/) BEPPU
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                                               product may be pBR322.
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ilarity 100.0%;
Conservative (
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                                 BP;
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                                                                                                                                                88JP-0302176
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                                                                       13pp;
                                                                                                                                                                                                                                                                                                                                                                                                           252 A;
                                                                                                                                                                                                                                             calf pro-rennin
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                                 252 A; 327
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 4.2%;
                                                                        Japanese
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0; Mismatches
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                                                                                        calf pro-rennin
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1e-14;
  DB 11;
1e-14;
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          Length 1098;
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                                                          system
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AAQ20949
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Matches 37
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                                                                                                                                                                                        Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prozennin derived sequence fused in phase with B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheese-making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding a polypeptide displaying milk clotting activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
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                                                                                                                                                                                                                                                               Recombinant DNA coding for milk clotting polypeptide -expressed in transformed bacteria % \left( 1\right) =\left\{ 1\right\} 
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P-PSDB; AAP40559.
                                                                                                                                                                                                                                                                                                                        Cashion LM,
                                                                                                                                                                                                                                                                                                                                        (CODO-) CODON GENETIC ENG
                                                                                                                                                                                                                                                                                                                                                          31-MAR-1983;
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                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1984.
                                                                                                                                                                                                                                                                                                                                                                                                               EP123928-A.
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        13-MAY-1992
                         AAQ20949;
                                          AAQ20949
                                                                                                                                                                        Sequence 1175 BP;
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                                                                                                                             l Similarity 75.5
37; Conservative
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                                            standard;
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                                                                                                                                                                                                                                               2; 39pp; English.
                                                                                                                                                                                                                                                                                                                        McCaman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant protein; rennet substitute; milk clot; ss
                                                                                                                                                                                                                                                                                                                                                                            84EP-0103551
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70..1166
/*tag= k
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                                                                                                                                                                         263 A; 355 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA;
                                           cDNA; 1175
                                                                                                                                     4.2%;
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                                                                                                                                                                                                                                                                                                                         Rice
                                                                                                                              12;
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                                                                                                                              Score 49; DB
Pred. No. 1e-1
12; Mismatches
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                                                                                                                                                                         238
                                                                                                                                       DB 5;
1e-14;
                                                                                                                                                                          U; 0 other;
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                                                                                                                                                Length 1175
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RESULT
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Best Local Similarity
""tches 37; Conserv
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12-DEC-1986;
31-MAR-1983;
28-APR-1986;
                                                                                                                                                                                                                                                                              specific clones were used to screen for recombinant plasmids. Only two clones 5G3 and 15C5 were found to contain the whole prorennin sequence, with clone 5G5 having its complete coding sequence (shown here). The sequence was the same as the published sequence except for two silent mutations in codons 274 and 336 respectively, and a single mutation in codon 302 which converts the sequence to the B form of rennin. The product of prorennin, rennin is an active component of rennet which is used to clot milk in the process of making cheese.
                                AAQ14051
                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA species, hybridisation with rennin specific probes was performed using probes derived from the published amino acid sequence of prorennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see AAQ33291,2). Reverse transcriptase was used to transcribe mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolating heterologous polypeptide from bacterial inclusion bodies - by lysing cells, extn. with nonionic detergent and sepg. insoluble polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                         Sequence 1175 BP; 261 A; 355
                                                                                                                                                                                                                                                                                                                                                                                                      into a cDNA copy which was inserted into plasmid pBR322 and cloned into E. coli strain K-12 MM 294 (ATCC 31446). The prorennin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The prorennin (prochymosin) sequence was obtd.from mRNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BERL-) BERLEX LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5082775-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prochymosin
                                                                                                        649
                                                                                                                   656 tgttctcggtttacatggacaggaatggccaggaagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-049149/06.
DB; AAR20730.
                                                                                                     uguucucgguuuacauggacaggaauggccaggagagcaugcucacgcu 697
                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calf's stomach (abomasum). To identify rennin-specific
                                                                                                                                                                                                                                                                       AAQ20950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 6; 21pp;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (prorennin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88US-0263927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88US-0263927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21..1158
/*tag= 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= prorennin
/note= "also known ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autocatalytic activation; pseudorennin;
                               DNA; 1210
                                                                                                                                                                           4.2%;
75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "also known as prochymosin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                12;
                                                                                                                                                                            Score 49; DB 13
Pred. No. 1e-14;
                               ВP
                                                                                                                                                                                                                                       Ç
                                                                                                                                                                                                                                         319
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calf.
                                                                                                                                                                                                                                       <u>ଜ୍</u>
                                                                                                                                                                                                                                       240 U;
                                                                                                                                                                                                                                       0
                                                                                                                                                                0,
                                                                                                                                                                                            Length 1175;
                                                                                                                                                                                                                                       other;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           milk;
                                                                                                                                                              0
                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                 RESULT
AAT03006
밁
                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                It was used as heterologous peptide/protein together with parts of the alpha-S1-casein gene in the proon. of DNA constructs. The heterologous peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland. See also AAQ14050, AAQ14774-77.
10-MAY-1994;
                            09-MAY-1995;
                                                                                    W09530739-A1
                                                                                                                 Mammalian sp
                                                                                                                                                              al-3; albino
                                                                                                                                                                                         Chymosin open reading frame
                                                                                                                                                                                                                        13-JUN-1996
                                                                                                                                                                                                                                                     AAT03006
                                                                                                                                                                                                                                                                                   AAT03006 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1210 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 21; 41pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA constructs for expressing protein in milk -contg. specific mammary gland transcription control region and signal sequence, providing high yield and easy prod. recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-304858/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP451823-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prorennin; alpha-S1-casein gene; insulin-like growth factor I; IGF-I; mammary gland; ss.
                                                         16-NOV-1995.
                                                                                                                                               neterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hartl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONE ) CONSORT ELEKTROCHEM IND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-1990;
11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rennin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                            643
                                                                                                                                                                                                                                                                                                                                                                         656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                           tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brem
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                               gene; expression;
                                                                                                                                                           mutant; light-regulated; Neurospora;
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
94US-0240372
                            95WO-US05716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90DE-4012526
90DE-4011751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0105702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278
                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α;
                                                                                                                                                                                                                                                                                   1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 C;
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 12;
Pred. No. 1e-14;
0; Mismatches
                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                               control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 T;
                                                                                                                                               chymosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1210;
                                                                                                                                                           bread mould;
                                                                                                                                               SS
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                           691
                                                                                                                                                                                                                                                                                                                                                                                       704
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AAT03005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological
                                            Beppu T,
Hidaka M;
                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid for expression of heterologous protein - contains albino promoter for light induced expression in filamentous fungi
           P-PSDB; AAP40078
                      WPI; 1984-258001/42
                                                                                                      09-MAR-1983;
                                                                                                                            07-MAR-1984;
                                                                                                                                                    17-OCT-1984.
                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                            02-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                   AAN40055;
                                                                                                                                                                                                                                                                                                                                                                                           AAN40055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-404108/51
                                                                                                                                                                                                                                                                                                                   Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1240 BP; 274 A; 374 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                             Prochymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   700
                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 tgttctcggtttacatggacaggaatggccaggaagagcatgctcacgct 704
                                                                                                                                                                                                                                                                        taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the host.
                                                       Uozumi
                                                                                                                                                                                                                                                                                                                    prochymosin gene
                                                                                                                                                                                                                                                                                             expression vector;
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                              /*tag= a
1245..1250
                                                                                                      83JP-0038439
                                                                                                                             84EP-0102451
                                                                                                                                                                                                                                      3..1130
                                                        Ŧ,
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                        Nishimori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                           1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                             E.coli trp operon; chymosin; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                        Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
le-14;
                                                        z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                       Kawaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
         The inventors claim isolated chymosin (rennin) and prochymosin generation calves, and plasmids conty. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-13061) The microorganisms transformed by the plasmid are also claimed.
                                                                                                                Isolated chymosin or rennin and prochymosin genes - which replicate in prokaryotic organisms, esp. Esche and organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                  13-APR-1983;
01-JUL-1982;
                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN30022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN30022 standard; DNA; 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1278 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from plasmid pBR322. Typically plasmid pCR501 is obtd. from pOCT The transcriptional direction of pOCT 3 is opposite to that of pOCT 2; it is clockwise in pOCT 2 (5' to 3') whereas counter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), or (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinant plasmids harboured by Escherichia coli strains deposited as FERM BP-262, -263 and -264. Any portion of the nucleotide sequence as described in AAN40055 can be used. Also claimed is a vector derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression plasmid comprising prochymosin gene and vector useful for transforming Escherichia coli for prochymosin prodn
                                                                                         Claim
                                                                                                                                                                                                          (GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                     03-NOV-1983
                                                                                                                                                                                                                                                                                                                             BE897201-A
                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                   microbial vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of veal chymosin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inventors claim the prochymosin gene comprising a nucleotide sence from (a) the 1st codon (GCT) to the 365th codon (ATC),
                                                                                                                                                                     1983-820813/47.
DB; AAP30013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 4.2%;
l Similarity 100.0%;
49; Conservative (
                                                                                        Page 33-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                    83US-0484539
82US-0394433
                                                                                                                                                                                                                                                                           83BE-0017731
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309
                                                                                      43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Α;
                                                                                                                                                                                                                                                                                                                                                       ผ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                         French.
                                                                                                                                                                                                                                                                                                                                                                                                                                               rennin; chymosin; cheese making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 5;
Pred. No. 1e-14;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                          plasmid(s)
                         (NRRL B-15061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                               genes
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RESULT 12
AAN30049
ID AAN300
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                                                                                                                                      RESULT
AAN91157
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                                                                                    Query match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                     The DNA encoding prochymosin can be cloned into a plasmid (esp. fros. cremoris SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome the shortage of prochymosin due to shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAN91158-N91160.
  AAN30049 standard;
                                                                                                                                                                                                                                          DNA fragment having region specifi is contained in plasmid in microor protein and food prodn. eg cheese.
                                                                                                                                      Sequence
                                                                                                                                                                                                                          Disclosure; fig 2; 43pp; Dutch.
                                                                                                                                                                                                                                                                                             WPI; 1989-030097/04.
                                                                                                                                                                                                                                                                                                                 Simons
                                                                                                                                                                                                                                                                                                                                                                         12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloned sequence of (pro)chymosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                   (NEZU-) NEDERL INS ZUIVELON
                                                                                                                                                                                                                                                                                                                                                      12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN91157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN91157 standard; DNA; 1291 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                          656 tgttctcggtttacatggacaggaatggccaggagaggcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                              NL8701378-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactic acid
                                                 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                              tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 671
                                                                                                                                                                                                                                                                                                                AFM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 4.2%;
1 Similarity 100.0%;
49; Conservative
                                                                                                                                                                                                                                                                                     AAP94144.
                                                                                                                                    1291 BP; 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1289
                                                                                    4.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pSK112;
                                                                                                                                                                                                                                                                                                                De Vos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP;
                                                                                                                                                                                                                                                                                                                                                      87NL-0001378
                                                                                                                                                                                                                                                                                                                                                                        87NL-0001378
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
29..1123
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-;prochymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310
  CDNA;
                                                                                                                                                                                                                                                                                                                 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS
                                                                                                                                     ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cheese; Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
   1314
                                                                                                                                     385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                    specific for lactic acid bacteria microorganism used in prodn. of
                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                    Score 49; DB 10;
Pred. No. 1e-14;
0; Mismatches
                                                                                                                                    Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
   ВP
                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ი</u>;
                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
1e-14;
                                                                                                                                    Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cremoris SK112; chymosin;
                                                                                     0;
                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1289;
                                                                                                      Length 1291;
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                                                                                    Indels
                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                    0
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                                                                                                                                   RESULT 13
AAN20043
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                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                               Preprochymosin is an intermediate (via prochymosin and pseudochymosin) for the enzyme chymosin, which is the essential milk-clotting component of rennet and is used in cheese manufacture. AAN30049 corresp. to mRNA isolated from the fourth stomach of a preruminant calf (abomasum, Frisian cow).
Key
                                                                                                                                                                                                                                                                                                                                                           DNA molecules comprising genes for preprochymosin - utransform microorganisms to give strain producing the prepro-enzyme and its allelic and maturation forms
                   Bos taurus
                                   Pre-pro-rennin; rennin;
protease; milk-clotting
                                                                                                      AAN20043;
                                                                                                                         AAN20043 standard; DNA;
                                                                                                                                                                                                                                                             Sequence 1314 BP;
                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1983-39656K/17.
P-PSDB; AAP30086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP77109-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence
                                                                 Pre-prorennin-A gene DNA sequence
                                                                                    16-DEC-1992
                                                                                                                                                                     Maat J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chymosin; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bovine preprochymosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN30049;
                                                                                                                                                                                                                        Local
                                                                                                                                                                                                              l Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNILEVER NV
                                                                                                                                                                                                                                                                                                                                                                                                                               Verrips CT,
                                                                                                                                                                                                             4.2%;
llarity 100.0%;
Conservative (
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82EP-0201272
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 24..40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                             309 A; 398 C; 338 G; 269 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rennet;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ledeboer
                                                                                                                         1460
                                    prorennin; enzyme;
enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cheese;
                                                                                                                                                                                                              0
                                                                                                                                                                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                               AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one of the allelic forms
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Edens
                                                                                                                                                                                                                       DB 4;
1e-14;
                                             EC-3.4.23.4;
                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                             0;
                                                                                                                                                                                                                               Length 1314;
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AC AAN4
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XX Yeas
XX Yeas
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XX Bos
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XX CB2!
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bases 1-204 and 1351 to 1460 are attached to the pre-prorennin but can be removed and are not essential to use of the gene in expression. The gene may be ligated into plasmid poGE21 and expressed in E. coli. The resulting expressed enzyume is a well known milk-clotting enzyme used in cheese-making.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1460 BP; 329 A; 440 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1982-62028E/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB2091271-A.
                                                                                    03-OCT-1984.
                                                                                                                                                                                                                   Yeast
                                                                                                                                                                                                                                           Sequence of
                                                                                                                                                                                                                                                                                         AAN40180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-1981;
                                                                                                           GB2137208-A.
                                                                                                                                                                                                                                                                 25-JAN-1992
                                                                                                                                                                                                                                                                                                                AAN40180 standard; cDNA; 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLB ) COLLABORATIVE RES INC
             (COLB ) COLLABORATIVE RES INC
                                   28-FEB-1983;
                                                           28-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                           833
                                                                                                                                                                                                                                                                                                                                                                                     656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                  taurus.
                                                                                                                                                                                                                                                                                                                                                                         tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 881
                                                                                                                                                                                                                   expression
                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells producing rennin and its precursors - recombinant {\tt DNA} material
                                                                                                                                                                                                                                         recombinant CGF4
                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mao J,
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81US-0325481.
81US-0225717.
                                   83US-0470911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82GB-0001120
                                                           84GB-0405129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205..1350
/*tag= a
/label=
/note= "pre-prorennin-A gene"
                                                                                                                                Location/Qualifiers
205..1350
/*tag= a
                                                                                                                                                                                                                   vector; GAL1 promoter; Saccharomyces cerevisiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (62028E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DΤ;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB; Pred. No. 1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                         carrying the rennin coding sequence
                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1460;
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AAN91188
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim a DNA segment contg. GAL1 promoter linked to gene - useful for direction of expression of the gene in yeast cell. The recombinant material carrying a GAL1 promoter of the yeast galactokinase gene may be used in expressing a desired protein, esp. bovine growth hormone, interferon, prorennin or preprorennin, in the yeast cell. Strains of Saccharomyces cerevisiae producing the polypeptides are produced. Yeast strains deposited as ATCC 20643, 20662, and 20663, strain designations CGY 196, 457, 461 and
                                                     Kluyveromyces host cells for producing polypeptide(s) - used for highly efficient prodn of eg chymosin tissue
                                                                                                                     van
                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                               AAN91188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1460 BP; 328 A; 440 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Table 4, Page 21-23; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    direction of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA segment contg. GAL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botstein D, Davis RW,
Mao JI, Moir DT, Gof
                      Disclosure; ;
                                                                                                                                        (KONN ) GIST-BROCADES NV
                                                                                                                                                                                   28-JUL-1988;
                                                                                                                                                                                                         01-JAN-1989
                                                                                                                                                                                                                             EP301670-A.
                                                                                                                                                                                                                                                                                          Kluyveromyces
                                                                                                                                                                                                                                                                                                               Kluyveromyces;
                                                                                                                                                                                                                                                                                                                                    BamHI/SalI insert of Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                         15-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                    AAN91188 standard; DNA; 2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                     656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                    den Berg
                                                                                     1989-033565/05.
DB; AAP94376.
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                                            activator or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                     JA,
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                      56pp;
                                                                                                                                                                                                                                                                                            lactis.
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                                                                                                                                                                87US-0078539
                                                                                                                                                                                    88EP-0201632.
                                                                                                                                                                                                                                                            Location/Qualifiers 409..1781
                                                                                                                     van Ooyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%;
                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fink
CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter linked to gene - of the gene in yeast cell
                                                                                                                                                                                                                                                                                                               chymosin;
                                            human
                                                                                                                       AJJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 5;
Pred. No. 1e-14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GR,
                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                            serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 G;
into plasmids pAB309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taunton-Rigby A,
                                                                                                                       Rietveld
                                                                                                                                                                                                                                                                                                                                    plasmid pAB309
                                                                                                                                                                                                                                                                                                               tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                            albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0;

BamHI/SalI insert,

incorporated

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CC primother; terminators and a d418 resistance marker fused to a ADHI CC promother from S. carevistae.
CC The Kluywarmwyces expression systems provide highly efficient secretion and processing of a vade variety of proteins.
CX Sequences identical to those published in gP30.669.
CX Sequence 2727 BP: 752 A: 654 C; 572 G; 749 T; 0 other;

Ouery Match
Best Local Similarity 100.0%; Pred No. 9.8e-15;
Best Local Similarity 100.0%; Pred No. 9.8e-15;
Astribus 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 655 igitrarighthroxygosapatygosapasagesteptaceget 704

DD 1268 tyltcrogyttlacatygacagaatygocagaagaagacsteptaceget 704

CS search completed: August 1, 2002, 01:57:49

Search completed: August 1, 2002, 01:57:49
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Minimum DB seq length: 0
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Perfect score:
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

     nucleic search, using sw model
                                                                                                                                                                            Match
                                                                                                                                                                                      Query
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Gapop 60.0 , Gapext 60.0
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1173
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gb_est2:*
gb_htc:*
gb_ss:*
gb_ss:*
em_gss_hum:*
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BG937697
BG938320
BG9387723
AV532492
O T20903
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   AV538262
AA9105042
AA411567
AV518232
AV559941
AA411566
AV536021
AI479358
AV518638
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AV548208
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AV532492 AV532492
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                                                                                                                                                             Mammalia; Eutheria; Cetartiodactyla; Bovidae; Bovinae; Bos.

1 (bases 1 to 383)

1 (bases 1 to 383)

Moore, S.S., Hansen, C., Li, C., Fu, A., I cDNA's from bovine abomasum tissue Unpublished (2001)

Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Ed Tel: 780 492 0169

Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                           sequence.
BG938086
BG938086.1
EST.
                                                                                                                                                                                                                                                                                                                                                BG938086
1Abo11A08
                                                                                                                 Email: smoore@afns.ualberta.ca
The sequence best matches qb:BPU19786 (Bos primigenius prochymosin mRNA, complete cds) in main database at high score of 735.0 and E-value of 0.0
PCR PRimers
                                                                           BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence
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                                                                            quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/clone_males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
                                                          Location/Qualifiers
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0 N27368
AV856918
AW749196
AW754326
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AIZ82510
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AV734647
AL7346493
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2 AQ896486
2 BQ8963689
AL667069
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0 AB8353509
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AL664439
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cDNA Library Bos
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AV53207 AV532027
AV542531 AV542531
AV439574 AV439574
AV542548 AV542248
AV542648 AV542248
AV542648 AV542248
AV537387 AV537387
BE037991 AA07D08 A
BE671871 7448f09.x
AQ084497 HS_2152-A
AV734647 AV734647
AV734647 AV734647
AV734647 AV734647
AU668938 AL668938
AQ896444 HS_3134 A
AG151623 Pan trog1
BH093689 RPCI-24-3
AU677069 AL667069
BE353509 EST353706
AV875590 AV875590
AV875590 AV875590
AV875590 AV875590
AV8756918 AL664431 AL664431
AV856918 AV856918
AW754327 CM1-CT033
AW754326 CM1-CT033
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AW754327 CM1-CT033
AW754327 CM1-CT033
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AW754328 CW0-CT033
AW754329 CW0-CT033
AW754329 CW0-CT033
AW754329 CW0-CT033
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CDNA 5', mRNA
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Canada

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BASE COUNT
ORIGIN
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                                                                     Query Match
Best Local
                                                       Matches
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656 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 704
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1Abo05E01
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49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA's from bovine abomasum
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                           Seq primer: T3 primer 
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                             The sequence best matches gb:BOVCHYMOA mrna)in main database at high score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COW
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                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
FORWARD: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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ilarity 100.0%;
Conservative (
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llarity 100.0%;
Conservative
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111 c 113 g 76 t
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I; Site_2: Xho I"
130 c 119 g 84 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:14337069
                                                                                                                                                                                                                                                                                                                                                                       Reverse
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                                                      Score 49; DB
Pred. No. 4.3
0; Mismatches
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Pred. No. 4.2e-14;
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n cDNA Library
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4.3e-14;
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5', mRNA
                                                       Gaps
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BG938320
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Best Local
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BG938320
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1Abo15E12
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49; Conserv
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 472)
Moore, S.S., Hansen, C., Li, C., Fu, A
cDNA's from bovine abomasum tissue
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovinae; Bos. 1 (bases 1 to 399)
                                                                                         EST.
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Seq primer: T3 primer
High quality sequence
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The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin)
mrna) in main database at high score of 928.0 and E-value of 0.0
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                                                             Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                              104
                                                                                                                                                                                                                                                                                                     4.2%; So lilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Epithelial"
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I; Site_2: Xho I"
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                         GI:14337095
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                                                                                                                                                                  399 bp
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No.
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4.4e-14;
thes 0;
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taurus
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CDNA 5', mRNA
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nes 43; Conserv
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Arabidopsis thaliana
Arabidopsis Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 325)
                                            Kazusa DNA Research Internation 292-0812, Japan Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                            DNA Res. 7, 175-180 (2000)
20363093
                                                                                                                                                                                                                  A large scale analysis of cDNA in Arabidopsis thaliana: of 12,028 non-redundant expressed sequence tags from nor size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV532492 325 bp mRNA linear AV532492 Arabidopsis thaliana flower buds Columbia thaliana cDNA clone FB043b03F 3', mRNA sequence. AV532492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                 The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                     AV532492.1 GI:8692775
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                                                                                                                                                            Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smoore@ains.ualberta.ca
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    /organism="Arabidopsis thaliana"
/strain="Columbia"
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/tissue_type="Gastrointestinal tissue
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Young adult"
/lab_host="XII-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95148729
On Jan 7, 1998 this sequence version
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1 (bases 1 to 339)
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2911 Lambda-PRL2 Arabidopsis
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                    67
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              /clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

13 others
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/Clone="FB043b03F"
/Clone_ilb="Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
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                                                                                                                                                                                                                                                    /clone="89F9T7"
                                                                                                                                                                                                                                                                       /strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis
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thaliana cDNA clone 89F9T7, mRNA
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Somerville,S., Thomashow,M., Retzel
                                                                                                                                                                                                                                                                                                               thaliana"
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AV538262.1 GI:8698545
EST
thale cress.
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AV538262 Arabidopsis thaliana roots Col
cDNA clone RZ113a03F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                       ch 2.0%;
l Similarity 100.0%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A large scale analysis of cDNA
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                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 391)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                   AA969042 391 bp mRNA linear EST 07-JUL-19-
op43d07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1579597 3' similar to TR:Q27951 Q27951 PROCHYMOSIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asamizu,E., Nakamura,Y.,
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                                                                                                                                                        AA969042.1
                                                                                                                                                                        AA969042
                                                                                                                                                                                      sequence.
Unpublished (1997)
                 Tumor Gene Index
                                                                                                                           human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="RZ113a03F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
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                                                                                                                                                          GI:3144222
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Pred. No.
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AA411567/c
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                                                                                                                                                                                                                                                                                                                       REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Query Match
Best Local Similarity
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 619 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 378.
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zv22g01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IM.
similar to SW:CHYM_SHEEP p18276 PROCHYMOSIN PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AA411567
AA411567.1 GI:2069151
                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 374.
                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 404)
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
                                                  Location/Qualifiers
                                 . 404
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 Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                           school of Medicine way, Box 8501, St. 1
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1.2;
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IMAGE:754416 3'
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REFERENCE
AUTHORS
TITLE
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AV518232/c
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MEDLINE
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Best Local
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AV518232 Arabidopsis thaliana
old Arabidopsis thaliana cDNA
AV518232
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DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eurosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of ,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                        XhoI
                                                                                                        /clone_lib="Arabidopsis thaliana aboveground
six-week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pregnant uterus"
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/db_xref="taxon:9606"
/clone="mAGE:754416"
/clone_11b="Soares_NhHMPu_S1"
/tlssue_type="pooled human melanocyte, fetal heart,
                                                                                                                                                /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="APD13d01F"
                                                              /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
                                          note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: mixed (see below); Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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100.0%; Pr
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Pred. No. 1.2;
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                                          Site_1:
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                                          EcoRI; Site_2:
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VERSION KEYWORDS

ACCESSION

Spoor

SOURCE

FEATURES

Score

23;

DB

9;

Length

408;

COMMENT

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ORIGIN

В

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KEYWORDS
SOURCE
ORGANISM
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KEYWORDS
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AV559941/c
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                                                         REFERENCE
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ORIGIN
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                                                                                                                                         VERSION
                                                                                                                                                          ACCESSION
                                                                                                                                                                                   DEFINITION
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MEDLINE
                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                       zv22g01.rl
similar to
AA411566
1 (bases 1 to 438)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,
, Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyl
,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV559941 411 bp mRNA linea AV559941 Arabidopsis thaliana green siliques Colthaliana cDNA clone SQ126c01F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia;
                                                                                                                             TST
                                                                                                                                                                                                   AA411566
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20363093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 12,028 non-redundant expressed sequence tags size-selected cDNA libraries
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1 (bases 1 to 411)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV559941.1 GI:8731367
EST.
                                                                                                 Homo sapiens
                                                                                                                                         AA411566.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba
Email: asamizu@kazusa.or.jp,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thale cress.
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/clone="SQ126c01F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis
/strain="Columbia"
                                                                     ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescriptII
                                                                                                                                                                 438 bp mRNA linear EST 17-MAY-19 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:754416 TR:G457097 G457097 CHYMOSIN C. [1];, mRNA sequence.
                                                                                                                                           GI:2069150
                                                                                                                                                                                                                                                                                                                                          2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                 109
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Primates;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292-0812,
                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               96
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                                                                                                                                                                                                                                                                                                                                                      Length 411;
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s Columbia Ar
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                                                                                                                                                                                   EST 17-MAY-1997
IMAGE:754416 5'
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COMMENT
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                                                                                                                                                                                                                                                                        AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV536021 Arabidopsis thaliana flower buds Columbia Arabidopsis thaliana cDNA clone FB106c09F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-Merck EST Project 1997
                                                                                                         Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 483)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV536021
AV536021.1 GI:8696304
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                                                                                                                                                                                               DNA Res. 7, 175-180
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                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mixed (see below); Vector: pT7T3D-Pac /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polyylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and sc circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5977315"
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/organism="Arabidopsis thaliana"
                                       Location/Qualifiers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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1.2;
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JOURNAL
COMMENT
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AUTHORS
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AI479358/c
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ORIGIN
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ORGANISM
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Best Local Similarity
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                                                       Query Match
Best Local
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 1015 ccctccgcctataccagccagga 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Towarth: 608 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1479358 505 bp mRNA linear EST 14-tm27e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157828 3' similar to TR:Q28950 Q28950 PREPROCHYMOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 505)
                                        l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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                                      2.0%;
ilarity 100.0%;
Conservative
                                                                                                                                              //note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBL) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 72996-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 367.
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/db_xref="taxon:3702"
/clone="FB106c09F"
/clone_lip-"Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
/tissue_type="flower buds"
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xhor"
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ISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

CE 1 (bases 1 to 51)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
AL DNA Res. 7, 175-180 (2000)
NE 20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers
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1 (bases 1 to 3957)
van Rooijen,G., Keon,R.G., Boothe,J. and Shen,Y.
Commercial production of chymosin in plants
Patent: WO 0114571-A 3 01-MAR-2001;
SemBloSys Genetics Inc. (CA)
Location/Qualifiers

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2400	. acagtgtcaccatcagcggtgtggttgttgcatgtgaaggtggatgtcaagctatcttgg 	2341	Db Qy
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2220 2220	tacctgtgtttgacaacatgatgaaccgacacctagtagctcaagacttgttctcggttt 	2161 2161	ДQ
2160 2160	atgcagaattcgatggcatccttggtatggcatacccatcgctcgc	2101	<b>р</b> у
2100 2100	ttgtggacattcaacagacagtaggacttagcacccaagaaccaggtgatgtcttcacct 	2041	рь
2040 2040	actacggtacaggtagcatgcaaggaatcttaggctatgataccgtcactgtctccaaca 	1981 1981	p 24
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Phaseolus vulgaris. Phaseolus vulgaris RESULT 2
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PHVBCSP 3502 bp DNA linear PLN 17-JUN-1998 Phaseolus vulgaris beta-type phaseolin storage protein gene, complete cds. J01263 M13758 J01263.1 GI:3228361

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tgagacacttcagggatgttc 3 	tttattttttatcagcaaagaataaataaaataliiiiiiiiiiiiiiiiiiiiii	3841 3841	Qу
accgtgtgcttagcttcttta 3 	cactacacataacccttttagcagtagagcaatggttg	3781 3781	Оy
otgcataatttatgcagtaaaa 37 	aggcaagggaaattttttaatttgggttgtcttgtttg 	3721 3721	g 99
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The glycosylated seed stor
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Station, TX 77843-3155,
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On Jun 16, 1998 this sequence version replaced
Location/Qualifiers
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van Rooijen,G., Keon,R.G., Boothe,J.
Commercial production of chymosin in
Patent: WO 0114571-A 1 01-MAR-2001;
SemBloSys Genetics Inc. (CA)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Sequence 2 1
Ax252300
Ax252300.1
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Hypoallergenic transgenic soybeans
Patent: WO 0168887-A 2 20-SEP-2001;
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1 (bases 1 to 2970)
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synthetic construct
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ilarity 100.0%;
Conservative
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/db_xref="taxon:32630"
/note="chimeric construct"
547 c 527 g 878 t
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                 DEVELOPMENT OF PLANT STRUCTURAL GENE
DEVELOPMENT OF PLANT STRUCTURAL GENE
PATENT: JP 1985210988-A 2 23-OCT-1985;
AGURIJIENETEIKUSU RES ASSOC LTD
OS Escherichia coli
PN JP 1985210988-A/2
PD 23-OCT-1985
PF 16-APR-1984 JP 1984077452
PF 16-APR-1983 US 83 485614
PI JIVON DELI KENPU, TEIMOSHII SHII HOC
PI DENISU DABURITU SARISUTON, NORIMOTO PC
C12N15/00, A01H1/00,C12N1/20,C12N5/00
PC C12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC anti-sense: No;
CC *source: library-plasmid pKS4-KB;
FH Key Location/Qualifiers
FH 5'UTR 1.177
FT CDS
FT 5'UTR 1.177
FT 5'UTR 1.177
FT 5'UTR 1.1768..1958)
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E00452
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Bacteria; Proteobacteria;
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15-APR-1983 US 83 485614
JIYON DEI KENPU, TEIMOSHII SHII HOORU,
DENISU DABURIYU SATSUTON, NORIMOTO MURA:
                                                                                                                                                                                                     C12N15/00, A01H1/00, C12N1/20, C12N5/00, (C12N1/20, C12R1:01),
 promoter
                                                                                                *source: library=plasmid pKS4-KB;
Key Location/Qualifiers
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/product='faseorin
101. .177
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Artificial sequence
A06496
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1 (bases 1 to 2090)

Kemp,J.D., Hall,T.C., Slightom,J.L.,

Plant structural gene expression

Patent: EP 0126546-A 24 28-NOV-1984;

LUBRIZOL GENETICS INC.
                                                                                                                                                                synthetic construct. synthetic construct
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                                                     /organism="Escherichia coli"
/db_xref="taxon:562"
416 c 372 g 588 t
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/product="phaseolin"
/protein_id="CAA00562.1"
/db_xref="GI:490412"
/translation="MMRARVPLLLLGILFLASLSASFATSLREEEESQDNPFYFNSDN
                                                                                                 Location/Qualifiers
                                   transl_table=11
                                            /codon_start=1
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842. .922
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1768. .1958
1958. .<2090.
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1047. .
1278. .
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Pred. No. 9.9e-77;
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phaseolin.
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                                                                                     Phaseolus vulgaris gene for alpha-phaseolin.

X52626

X52626.1 G1:20972

alpha-phaseolin; glycoprotein; phaseolin; seed storage protein.

phaseolus vulgaris.

Phaseolus vulgaris

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae.
Anthony,J.L.
Direct Submission
Submitted (17-APR-1990) Antony J.L., Dept. of Biology,
University, College Station, TX 77843-3258, USA
2 (bases 1987 to 4764)
                                                                                Phaseolus.
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llarity 100.0%;
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RSGSALIVLVKRDDRREYFFLTSDNP1FSDHQKIPAGTIFYLVMPDPKEDLRIIQIAN
PVNNPQIHEFFLSSTBAQQSYLQEFSKHILBASFNSKPEELINEVLFEEBGQGEGVYUN
IDSEQIKELSKHAKSSSRKSLSKQDNTIGNEFGNLTERTDNSLNVLISSIEMEEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAAXPVAI
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754..841
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1665. .176
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1278. .14
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923. .1046
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423 c
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1047. .1277
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1768. .>1958
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Pred. No. 9.8e-77;
0; Mismatches 0;
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Best Local Sin
Matches 269;
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TITLE
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                                                                                                               catgcatgttccaaccaccttctctcttatataatacctataaatacctctaatatcact 1466
                                                                    aatttottcacttcaacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctc 1406
CATGCATGTTCCAACCACCTTCTCTCTTATATACCTATAAATACCCCTAATATCACT
                                                      AATTTCTTCACTTCAACACACGTGAACCTGCATATGCGTGTCATCCCATGCCCAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthony, J.L., Vonder Haar, R.A. and Hall, T.C. Nucleotide sequence of an alpha-phaseolin g \in \mathbb{R}
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nilarity 99.3%;
Conservative
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4084. .4137
/note="repeat region"
a 897 c 782 g
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/translation="MMRARVPILLLGILFLASLSASFATSLRBEEEESQDNPFYFNSDN
SWNTLFKNYGVEHIRLLGFEDQDSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVV
RSGSAILVLVKPDDRREYFFLYSDNPIFSDHQXIPAGTIFYLVNPDPKEDLRIIQLAM
PVNNPQIHDFFLSSTEAQOSYLQEFSKHILEAASFNSKFEEINRYLFAREGQDEGVIVN
IDSEQIEELSKHAKSSKSKSLSKQDNTIGNEFGNLTERTDNSLNVLISSEMKEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKONKETLEYESYRAELSKDDVFYIPAAYPVAL
KATSNVNFTGFGINANNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGEEVMKL
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3221. .345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="alpha-phaseolin"
/protein_id="CAA36853.1"
/db_xref="GI:295832"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2737
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3580. .3838,3942. .4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="leaf"
2196. .2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sanilac"
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                                                                                                                                                                          Score 169; DB 8; Length 4764;
Pred. No. 6.2e-71;
0; Mismatches 2; Indels
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PVPHASBR
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                                                VERSION
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Best Local Sim.
Matches 133;
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TITLE
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                                                                                                                                                                                                                                                                                                                        aataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgt 2791
                                                                                                                                                                            AGGATGTTATGAT 1475
                                                                                                                                                                                                         aggatgttatgat 2864
                                                                                                                                                                                                                                                                                                         AATAAGTATGAACTAAAATGCATGTAGGTGTAAGAGCTCATGGAGAGCATGGAATATTGT 1402
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                                                                                                                                                                                                                                         ATCCGACCATGTAACAGTATAATAACTGAGCTCCATCTCACTTCTTCTATGAATAAACAA 1462
                              x03004.1 GI:21039 glycoprotein; phase
storage protein.
Phaseolus vulgaris
                                                              Phaseolus vulgaris mRNA X03004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artificial sequence.

1 (bases 1 to 1475)

Kemp,J.D., Hall,T.C., Slightom,J.L.,
Plant structural gene expression
Patent: EP 0126546-A 33 28-NOV-1984;
LUBRIZOL GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Al1822
Artificial mRNA for phaseoline.
Al1822
Al1822.1 GI:491197
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synthetic construct
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Similarity 100.0%;
33; Conservative (
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SWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVV
RSGSALILVLYKEDDRREYFFLYSDNP1FSDHQXIPAGTIFYLVHDDPKEDLR1IQLAM
PVNNPQIHEFFLSSTEAQQSYLQEFSKH1LEASFNSKFEEINRVLFEEEGQQEGVTV
IDSEQIKELSKHAKSSSRKSLSKQDNTIGNEFGNLTEBTDNSLNVL1SSIEMEEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAAYPVAI
KATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INKQSGSYFVDAHHHQQEQQKGRKGAFVY"
334 c 306 g 380 t
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/protein_id="CAA00988.1"
/db_xref="GI:491198"
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78. 1345
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/transl_table=11
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                               phaseolin;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                     Score 133; DB 6;
Pred. No. 2.6e-53;
0; Mismatches 0;
                                                                             for beta-type
                                                                                               1475
                              seed storage protein; signal peptide;
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                                                                           mRNA linear
pe phaseolin.
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                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                            NTd
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REFERENCE
AUTHORS
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Best Local S
Matches 133
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                                                                                                                                 Local Similarity
atccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The single base deletion in a variant clone can be due cloning artefact or to a represented pseudogene.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slightom,J.L., Drong,R.F., Klassy,R.C. and Hoffman,L.M. Nucleotide sequences from phaseolin cDNA clones: the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phaseolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 13 (18), 6483-6498 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins from Phaseolus vulgaris are encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [amilies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1475)
                                                                                                                                                                                                                 455
                                                                                                              3.4%; Score 133; DB 8; ilarity 100.0%; Pred. No. 2.6e-53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT: P02853"
/translation="MMRARVPLLLIGILFLASLSASFATSLREEEESQDNPFYFNSDN
/translation="MMRARVPLLLIGILFLASLSASFATSLREEEESQDNPFYFNSDN
/translation="MMRARVPLLLIGILFLASLSASFATSLREEEESQDNPFYFNSDN
SWNTLFKNQYGHIRVLQREDQXSKRLQNLEDYRLVEBRSKPETILLLPQQADABLLLVV
RSGSAILVLVKFDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIIQLAM
PVNNPQIHEFFLSSTEAQQSSLQEFSKHILEASFNSKFEEINKVLFEEEGQQEGVIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPHYYSKAIVILVVNEGEAHVELVGPKONKETLEIESVRAELSKODVFUPAAVEVAI
KATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKL
INKQSGSYFVDAHHHQQEQQKGRKGAFVY"
                                                                                                                                                                                                                                               /note="put.
1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="mature beta-phaseolin (aa 1-398)"
149. .150
                                                                                                                                                                                                                                                                                                                                               and premature stop 831. .839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA26789.1"
/db_xref="GI:21040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Phaseolus vulgaris"
/db_xref="taxon:3885"
                                                                                                                                                                                                                /note="polyadenylation site"
335 c 306 g 379 t
                                                                                                                                                                                                                                                                                 1454. .1458
                                                                                                                                                                                                                                                                                                               1098.
                                                                                                                                                                                                                                                                                                                                                                             /note="A is missing
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155. .156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="cap site in variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="cap site"
L. .1475
                                                                                                                                                                                                                                                                                              1098. .1106
/note="pot.
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                                                                                                                                                                                                                                                                                                                             note="pot. glycosylation site"
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153
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EMBO J. 6, 3213-3221 (1987)
This sequence is a chimera between Phaseoleus vulgaris sequences
from J.L. Slightom, S.M. Sun and T.C.Hall (1983) 'Complete
nucleotide sequence of a French bean storage protein gene:
phaseolin', Proc. Natl. Acad. Sci USA 80:1897-1901, and Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 207)
Hoffmann, L.M., Donaldson, D.D., Bookland, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays/P.vulgaris
X06175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K. Pedersen, P. Argos, S.V.L. Naravana and B.A. Larkins (1986)
'Sequence analysis and characterization of a maize gene encoding
high-sulfur zein protein of Mr 15,000',
J. Biol. Chem. 261:6279-6284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences from
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                                                                                                                                                                         Similarity
                                                                                                                                                     2.4%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                      /note="zein transcription initiation
161. .>207
161. .>207
                                                                                                                                                                                                                                                                                                        /product="chimeric beta-phaseolin/zein"
/protein_id="CAA29542.1"
/db_xref="GI:22547"
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/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                       translation="MKMVIVLVVCLALSAA" 60 c 33 g 53 t
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a; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               direct repeat; glycoprotein; phaseolin; seed st
signal peptide; storage protein; tandem repeat.
phaseolus vulgaris.
phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The variability in transcription initation may be due to multiple and overlapping TATA-elements in the genomic sequence (see <PVPHASL>). Seven slightly different alpha-phaseolin cDNA clones were detected. Whether the differences represent nucleotide substitutions in allelic genes or show divergences of non-allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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x02980.1 GI:21035
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                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MMRARVPLLLIGILFLASLSASFATSLREEEESQDNPFYFNSDN
SWNTLEKNQYCHIRVLQRFDQQSKRLQNLEDYRLVEERSKPETLLPQQADAELLLVV
RSGSAILVLVKPDDRREYFFLTQGDNPIFSDNQKIPAGTIFYLVNPDPKDDAELLLVV
RSGSAILVLVKFDDRREYFFLTGGDNPIFSDNQKIPAGTIFYLVNPDEKEDDREILIQLA
MPVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEGQOEEGQ
EGVIVNIDSEQIEELSKHAKSSSRKSHSKQDNTIGNEFGNLTERTDNSLNVLISSIEM
KEGALEVPHYYSKAIVILVVNEGEAHVELVGFPKNKETLEFESYRAELSKDDVFVIPA
AYPVAIKATSNVNFTGFGINANNNNRULLAGKTDNVISSIGRALDGKDVLGLTFSGSG
EEVMKLINKQSGSYFVDGHHQQEQQKGSHQQEGQKGRKGAFVY"

87. 155
486. .488
/note="AAC (Asn) is
533
                                                                                                 /note="ACGCAAGGC variant clones" 456. 464
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339
                                                                                                                                                                                                                                                /note="pot. altern.
164. .165
                                                                                                                                                                                                                                                                                                                                 /product="put. mature alpha-phaseolin (aa 1-413)"
158. .159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA26718.1"
/db_xref="GI:21036"
/db_xref="SWISS-PROT:P07219"
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/db_xref="taxon:3885"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 2.3%; l Similarity 100.0%; 90; Conservative
                                                                                                                                                               Submitted (30-AUG-1993) James A. Ki University of California at Davis,
                                                                                                                                                                                                                                              Kami.J.A. and Gepts,P.
Phaseolin nucleotide sequence diversity in Phaseolis vulgaris (Genome 37, 751-757 (1994)
                                                                                                                                                                                                                                                                                                                                Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                           Kami, J.A.
                                                                                                                                                                                                                                                                                                                                                                                          French bean.
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Phaseolus vulgaris
                                                                                                                                                                                                                                     95095072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cds
                                              /map="linkage group D7"
/clone="Sanilac 1-12"
/hapolotype="\S' type beta-phaseolin"
/tissus type="cotyledge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="polyadenylation sites 344 c 323 g 388 t
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1530
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858. .866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="GAA (Glu) is GAC 711. .725
                        /tissue_type="cotyledon"
/clone_lib="Sanilac pUC19 cDNA"
                                                                                                         /organism="Phaseolus vulgaris"
/cultivar="Sanilac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="direct repeat 2" 1509. ,1514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="C is T in 594. .596
             /dev_stage="cotyledonary stage"
                                                                                            /db_xref="taxon:3885"
                                                                                                                                                  Location/Qualifiers
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726. .740
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Sanilac clone 1-12 phaseolin
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Pred. No.
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                                                                                                                                                               . Kami, Agr
is, Davis,
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(Phs) mRNA,
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USA
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Best Local Similarity 100.0%;
Matches 77; Conservative
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              Maize chimeric zein/beta-phaseolin
X06176
X06176.1 GI:22548
phaseolin;
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/phenotype="'T' type phaseolin"
/replace="gasgasgsgacascasgasgsgasgsacascaa"
/product="phaseolin"
807..815
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1429. .1434
/gene="Phs"
a 324 c
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/product="phaseolin"
/product="criphaseolin"
/protein_id="AAA99534.1"
/db_xref="GI :403594"
/db_xref="GI :403594"
/translation="myraryplumiligilflasisasfatsireeeesodnpfyfnsdn
/translation="myraryplumiligilflasisfatsfxpetilipopareilityV
swntlfknqyghirvlordqoskriqnledyrlvefrspepereilitylam
FVNNPQIHDFFLSSTEAQQSYLQEFSKHILEASFNSKFETINRVLFEEEGQQEGV'UN
IDSEQIKELSKHAKSSSRKSIJSKQDNYIGNEFGNLTERTDNSIJNVLISSIEMKEGALF
VPHYYSKAIVILVVNEGEAHVELVGPKGNKETILEYESYRAELSKDDVFVIPAAYPVAI
KATSNVNFTGFGINANNNNNILLAGKTDNVISSIGRALDGKDVIGLTFSGSGDEVMKL
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/gene="Phs"
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/product="phaseolin"
674. .679
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1271. .1298
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123. .1316
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54. .1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="\T'
/label=27bp-repeat
/phenotype="\T' type
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                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phaseolin"
1320. .1454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="putative glycosylation
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                                                                                                                                                                                                                                                                                Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type phaseolin"
                                                                348
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                                                gene 3'end region
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                                                                linear
                                                                PLN 06-AUG-1992
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REFERENCE
AUTHORS
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MEDLINE
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AUTHORS
TITLE
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ORGANISM
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JOURNAL
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Best Local
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Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae; PACC

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic tobacco seeds
EMBO J. 6, 3213-3221 (1987)
Location/Qualifiers
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                                                                                                                                                                                                                                                                         001121 1478 bp mRNA
Phaseolus lunatus phaseolin (Phs) mRNA,
001121
U01121.1 GI:403581
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            Direct Submission submitted (30-AUG-1993) James A. Kami, Agronomy and Range Science University of California at Davis, Davis, CA 95616, USA
                                                                                                             Kami,J.A. and Gepts,P.
Phaseolin nucleotide sequence diversity in Phaseolus.
Intraspecific diversity in Phaseolus vulgaris
                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                         Kami, J.A.
                                                                                                 Genome 37, 751-757 (1994)
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Similarity 100.0%;
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                                                                                     5095072
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253. .25
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/db_xref="taxon:4577"
<1. .269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="pot.polyA site"
340
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298. .303
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93 c 62 g :
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 Location/Qualifiers
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.241
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258
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      1478 bp
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3. 5.9e-25;
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Search completed: August 1, 2002, 01:42:21 Job time: 16831 sec
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Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 63; Conservative 0; Mismatches 0;
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                                                                                    TGA 64
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1457. .1462
/gene="Phs"
a 340 c
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133. .1344
/gene="Phs"
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/product="phaseolin"
/protein_id="aaa99532.1"
/protein_id="aaa99532.1"
/db_xref="GI:403582"
/translation="mmrarvpllligilf-lasisasfaislrehnesodnpeyfssbn
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RSGSALLALVKFOGTIIYSLKQDDTLKIPAGTIFFLINFQNNEDLRIIKLAMTVNNQ
IQDFFLKSTEAQOSYLYGFRKDILDASFNSPIEEINRLLFAEEGORGEVIVNIGSDLI
QELSRHAKSSSRKSLDHNSLDISNEWGNITDIYVNSLDVFVIPAATVPEIKEGGLFVPHYNS
KAIVILVVEEGVAKVELVGFKREKESLELETYRADVSEGDVFVIPAATKAISNNV
MFTSFGINANNNYRILLTGKGGPTGKEDNIISAGINDVLGLMFPGSGEDVQKLFNNO
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/gene="Phs"
61. .1347
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1063. 1071
/gene="phs"
/function="putative glycosylation site"
1237. 1245
/gene="phs"
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                                                                                                                                                                                                                                                                                                                                                                                             /function="putative glycosylation site"
1255. 1263
/gene="phs"
/function="putative glycosylation site"
1348. 1478
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/gene="Phs"
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/product="phaseolin"
151. .159
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/strain="G25804"
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/function="putative
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/clone_lib="G25 pUC19 cDNA"
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

98755AW2P	Result
3957 1544 1439 1226 1173 887 49	Score
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Bovine phaseolin p Nucleotide sequenc Phaseolus vulgaris Nucleotide sequenc Bovine pre-pro-chy Kunitz soybean try Sequence of proren Sequence encoding	Description

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immune		Tumour suppressor	Chemically pretrea	Chemically pretrea	Human immune syste	Cryptosporidium pa	Human digestive sy	Human pancreatic c	Drosophila melanog	dopsis tha	Human aspartyl pro	Arabidopsis thalia	PCR primer used to	Phaseolin gene pro	Sequence of recomb	Pre-prorennin-A ge	Rennin - casein co	DNA encoding His-c	ing for	Sequence coding fo	DNA encoding the f	Prochymosin gene 5	Sequence of prepro	BamHI insert from	2.7 Kbp HindIII fr	BamHI/SalI insert	Sequence of recomb	Pre-prorennin-A ge	cDNA sequence corr	Cloned sequence of		Sequence of prochy	Chymosin open read	Rennin gene. Synt	Prochymosin (prore

## ALIGNMENTS

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RESULT
AAS00570
Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thailana; potato; flax; linseed; rice; safflower; oll palm; ground nut; Brazil nut; coconut; castor; corlander; squash; jojoba; ds; phaseolin; promoter; terminator; mutant; French bean.
                                                                                                                                                                                Chimeric -
Chimeric -
                                                                                                                                          promoter
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                                                                                                                                                                                                                                                                                                  Bovine phaseolin promoter pre-pro-chymosin-phaseolin terminator.
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                                                             /*tag= b
/product= "Bovine pre~pro~chymosin"
2727...3957
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/note= "Phaseolin promoter"
1554..2726
                                   /*tag= c
/note= "Phaseolin terminator"
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220	tacctgtgtttgacaacatgatgaaccgacacctagtagctcaagacttgttctcggttt 22	Db 2161	
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160	augeagaattegauggeateettggtatggeataceeateggteeggegteagagtactega 21	Db 2101	
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00 0	anagattogatcogagaaagtogtccaccttocagaacttaggcaaacccttgtctatac 1	192	
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                                                                                                                                                                 The present sequence represents the bean phaseolin promoter, which CC is used to construct plasmids for the expression of the P. putida CC faoAB gene. The gene encodes an enzyme that may be used in the CC method of the invention. The specification describes a method for CC manipulating the metabolism of a plant, and comprises expressing a CC heterologous gene encoding fatty acid oxidation enzymes in the CC cytosol or plastids other than the peroxisomes glyoxisomes or CC mitochondria of the plant. The method may be used to enhance the CC biological production of polyhydroxyalkanoates or novel oil compositions CC in a transgenic plant. Plants which may be used to produce these CC compounds in this way include Brassicas, maize, soybean, cottonseed, CC sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco and CC sunfla. The method may also be used to prevent or suppress seed CC production and therefore increase the production of biomass (leaves, xxx etc.)
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Best Local Similarity 99.9
Matches 1539; Conservative
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                                                                                                        Fao gene; plant metabolism; fatty acid polyhydroxyalkanoate; oil composition; transgenic plant; terminator; bean; ss.
WPI; 1999-540850/45
           Boynton L, Snell K;
                                                                                                                                                                      AAZ10392
                                          06-MAR-1998;
                                                       05-MAR-1999;
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Modifying ng fatty acid metabolism and producing specific p n in plants, polymers in useful seeds for increasing

Example English.

The present sequence represents the bean phaseolin terminator, which is used to construct plasmids for the expression of the P. putida faoAB gene. The gene encodes an enzyme that may be used in the method of the invention. The specification describes a method for manipulating the metabolism of a plant, and comprises expressing a heterologous gene encoding fatty acid oxidation enzymes in the cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant. The method may be used to enhance the biological production of pollyhydroxyalkanoates or novel oil compositions in a transgenic plant. Plants which may be used to produce these compounds in this way include Brassicas, maize, soybean, cottonseed, sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco alfalfa. The method may also be used to prevent or suppress seed production and therefore increase the production of biomass (leaves, stems, stalks) by plants. and

Sequence 1244 BP; 456 A; 174 Ç 178 G; 436 T; 0 other;

Query Match 31.0%; Best Local Similarity 100.0%; Matches 1226; Conservative

31.0%;

0;

Score 1226; Depred. No. 0; Mismatches

DВ

20;

0;

Indels Length

0;

Gaps

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RRESULT
AASOLT
AASOLT
AC AASO
XX AASOL
XX BOVI
XX BOVI
XX Chym
KW PICE
KW Squal
XX Squal
XX Chym
KW Squal
XX Squal
XX IS IS
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                                                                                                                                                                                      Chymosin; transcription regulator; terminator sequence; soybean; corn; pre-pro-chymosin; rape seed; sunflower; cotton; tobacco; alfalfa; wheat; barley; oats; sorghum; Arabidopsis thallana; potato; flax; linseed; rice
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The patent discloses hypoallergenic transgenic soybeans and recombinant CC expression constructs to lower soybean vacuolar protein, commonly known CC as P34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA, CC Gly m IB, rGLY m3 or Glycinin Gl (alaBlb). The allergen content of the CC soybean is reduced by sense suppression which is accomplished by using CC the expression construct that comprises a nucleic acid fragment encoding CC transgenic soybean plants which can be used to make hypoallergenic CC transgenic soybean plants which can be used to make hypoallergenic copbean products which can be used to make hypoallergenic CC formulas) and animal feed applications. The oil made from seeds of the hypoallergenic transgenic soybean plants can be used as ingredients, CC as coatings, as salad oils, as spraying oils, as roasting oils. The foods in which the oil made be used include crackers and snack foods, confectionery products, syrups and toppings, sauces, CC batter and breading mixtures, baking mixes and doughs. The present CC cor KTi3), a minor soybean seed allergen.
                                                                                                                                                                                                                                                                                                                                                                                 Recombinant expression construct to lower allergen (e.g. content of a soybean, comprises a nucleic acid fragment allergen, useful for producing soybean plants which can be allergen.
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                       The inventors claim recombinant plasmids contg. the cDNA of calf prorennin. Specified plasmids are pCR 10001 and pCR2001 (contg. the whole sequence plus the lac promoter region). Also new are microorganisms transformed with the plasmids, esp. E. coli CR1 (ATCC property of the plasmids).
                                                                                                                                                                                                                                                                                                                          Sequence of prorennin
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                                                                                               Plasmid contg. calf
                                                                                                                                                            (BEPP/)
                                                                                                                                                                               24-AUG-1981;
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DB; AAP30603.
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                contg. plasmid pCR2001.
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                                                                                                                                           Uozumi T,
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                                                                                                                                                                                                                                                                                                         enzyme;
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                             Bos taurus
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                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT
AAQ20949
                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 37
28-OCT-1988;
11-MAY-1984;
12-DEC-1986;
31-MAR-1983;
28-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                              Also claimed is E.coli JM83/pLC7 (ATCC 39325) which is transformed with pLC7 contg. the prorennin derived sequence fused in phase wit B-galactosidase. The pLC7 prorennin expression plasmid includes sequences which code for both the pseudorennin and mature rennin cleavage sites between AAs 28-29 and AAs 42-43, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cashion LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP123928-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAP40559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1984-277277/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CODO-) CODON GENETIC ENG
                                                   28-OCT-1988;
                                                                                                                                                          Bos
                                                                                                                                                                                                 Prochymosin (prorennin) gene from calf.
                                                                                                                                                                                                                                                      AAQ20949 standard; cDNA; 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in transformed bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA coding for milk clotting
                                                                     21-JAN-1992
                                                                                      US5082775-A
                                                                                                                                                                          clotting
                                                                                                                                                                                                                     13-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1175 BP; 263 A; 355 C; 319 G;
                                                                                                                                                                                                                                                                        10
                                                                                                                                                          taurus.
                                                                                                                                                                                                                                                                                                                                   1.2%; l Similarity 75.5%; 37; Conservative
                                                                                                                                                                           activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCaman MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                     (first entry)
88US-0263927.
84US-0609495.
86US-0940199.
83US-0480860.
86US-0856700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83US-0480860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84EP-0103551
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70..1166
/*tag= l
                                                    88US-0263927
                                                                                                      /product=
/note= "al
                                                                                                                                 Location/Qualifiers 21..1158
                                                                                                                                                                                    autocatalytic
                                                                                                                         /*tag=
                                                                                                                                                                             ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ь
                                                                                                      "also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice
                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                   Score 49; DB
Pred. No. 1.4e
l2; Mismatches
                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CM,
                                                                                                                                                                                    activation;
                                                                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sias
                                                                                                                                                                                                                                                                                                                                            DB 5; 1
                                                                                                      prochymosin"
                                                                                                                                                                                                                                                                                                                                                                              238 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SR;
                                                                                                                                                                                    pseudorennin;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                   Length 1175
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       in phase with
                                                                                                                                                                                     milk;
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into a cDNA copy which was inserted into plasmid pBR322 and cloned into E. coli strain K-12 MM 294 (ATCC 31446). The prorennin specific clones were used to screen for recombinant plasmids. Only two clones 5G3 and 15C5 were found to contain the whole prorennin sequence, with clone 5G5 having its complete coding sequence (shown here). The sequence was the same as the published sequence except for two silent mutations in codons 274 and 336 respectively, and a single mutation in codon 302 which converts the sequence to the B form of rennin. The product of prorennin, rennin is an active component of rennet which is used to clot milk in the process of making cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The prorennin (prochymosin) sequence was obtd.from mRNA from unweaned calf's stomach (abomasum). To identify rennin-specific mRNA species, hybridisation with rennin specific probes was performed using probes derived from the published amino acid sequence of prorennin (Foltmann et al., J. Biol. Chem. 254, 8447-8456 (1979)) (see AQ23291,2). Reverse transcriptase was used to transcribe mRNA (see AQ23291,2).
                                                                          19-APR-1990;
11-APR-1990;
                                                                                                                                                                                                                                   Prorennin; alpha-S1-casein gene; insulin-like growth factor I; IGF-I;
                                                                                                                                                                                                                                                             Rennin gene
                                                                                                                                                                                                                                                                                                                                             AAQ14051 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     podies - by lysing cells,
insoluble polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-049149/06.
                       Hartl P,
                                                                                                                                                                     EP451823-A
                                                                                                                                                                                                                        mammary gland;
                                                                                                                                                                                                                                                                                         06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BERL-)
                                                                                                                  10-APR-1991;
                                                                                                                                           16-OCT-1991
                                                (CONE ) CONSORT ELEKTROCHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                            649 uguucucgguuuacauggacaggaauggccaggagagcaugcucacgcu
                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BERLEX LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g heterologous polypeptide from bacterial inclusion by lysing cells, extn. with nonionic detergent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ20950.
                       Brem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                          SS.
                        <u>ن</u>
                                                                          90DE-4012526.
90DE-4011751.
                                                                                                                 91EP-0105702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
                                                                                                                                                                                                                                                                                                                                             DNA; 1210
                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 13;
Pred. No. 1.4e-11;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>େ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detergent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sepg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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0;

WPI; 1991-304858/42

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AAT03006
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Best Local
The DNA is that of a mammalian gene (open reading frame) encoding chymosin. The gene was placed in operable linkage with the al-3 promoter (see AATO3005). The al-3 gene controls the production of geranyl geranyl pyrophosphatase (GGPP) synthetase. GGPP is a precursor for carotenoids and xanthophylls. It has been shown that exposure to light increases the transcription level of GGPP synthetase 15-45 fold. Light activates a number of genes in the common bread mould, Neurospora. This can be used to regulate the expression of genes encoding heterlogous proteins, e.g. chymosin, in recombinant production systems. Use of a light-regulated promoter is a simple and effective way to control expression and allows timing to be adapted to the physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2209 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 2257
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid for expression of heterologous protein - containable of promoter for light induced expression in filamentous
                                                                                                                                                                                                                                                                                                                                                                                             albino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-404108/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al-3; albino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chymosin open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT03006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1210 BP; 278 A; 356 C; 324 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-S1-casein gene in the produ. of DNA constructs. The heterologous peptide/protein together with parts of the peptide or protein may also be human insulin-like growth factor I. The constructs provide high yields of the protein with simple recovery from the milk. Activation of the gene occurs only in the mammary gland. See also AAQ14050, AAQ14774-77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA constructs for expressing protein in milk - contg. specific mammary gland transcription control region and signal sequence, providing high yield and easy prod. recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9530739-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian sp
                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stuart
                                                                                                                                                                                                                                                                                                                                     Fig 7; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 21; 41pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutant; light-regulated; Neurospora; bread
gene; expression; control; chymosin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0240372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US05716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame
                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 12; Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mould;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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2209 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 2257

Query Match Best Local Matches

Similarity

1.2%; 5cc 100.0%; Pr

Score 49; Pred. No.

DB 1.4e-11; S

Length 1278;

Indels

0;

Gaps

0

Mismatches

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                           The inventors claim the prochymosin gene comprising a nucleotide sequence from (a) the 1st codon (GCT) to the 365th codon (ATC), or (b) the 5th codon (CGG) to the 365th codon (ATC); and recombinant plasmids harboured by Escherichia coli strains deposited as FERM BP-262, -263 and -264. Any portion of the nucleotide sequence as described in AAN440055 can be used. Also claimed is a vector derived
Sequence 1278 BP;
                             from plasmid pBR322. Typically plasmid pCR501 is obtd. from pOCT The transcriptional direction of pOCT 3 is opposite to that of pOCT 2; it is Clockwise in pOCT 2 (5' to 3') whereas counter
                                                                                                                                        Disclosure; Fig 1; 59pp;
                                                                                                                                                           Expression plasmid comprising prochymosin gene and vector - useful for transforming Escherichia coli for prochymosin pr
                                                                                                                                                                                                                                                                                   09-MAR-1983;
                                                                                                                                                                                                                                                                                                         07-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2209 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct 2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1240 BP;
                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                               Hidaka
                                                                                                                                                                                                                                        Beppu T,
                                                                                                                                                                                                                                                             (BEPP/) BEPPU T.
                                                                                                                                                                                                                                                                                                                              17-OCT-1984
                                                                                                                                                                                                                                                                                                                                                  EP121775-A.
                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prochymosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN40055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN40055 standard; DNA; 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 tgttctcggtttacatggacaggaatggccaggagagcatgctcacgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                        1984-258001/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
49; Conserv
                                                                                                                                                                                              AAP40078
                   in poct
                                                                                                                                                                                                                                         Uozumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; So litarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prochymosin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression vector; E.coli trp operon; chymosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                    83JP-0038439
                                                                                                                                                                                                                                                                                                        84EP-0102451
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1245..1250
/*tag= b
                                                                                                                                                                                                                                         H
                                                                                                                                                                                                                                                                                                                                                                                                       3..1130
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 A;
                                                                                                                                                                                                                                         Nishimori
A;
                                                                                                                                         English.
384 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                        ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339
326 G;
                                                                                                                                                                                                                                        Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16,
3. 1.4e-11;
0;
 259
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0 other;
                                                                                                                                                                                                                                       Kawaguchi
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RESULT 15
AAN91157
ID AAN911
XX
AC AAN911
XX
DT 07-JUN
XX
Cloned
XX
KW Lactic
KW protei
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                                                                                                                                                                                                 Query Match 1.2%; Sometimes 1.2%; Sometimes 1.00.0%; Matches 49; Conservative 0;
                                                                                                                                                                                                                                                                    rne inventors claim isolated chymosin (rennin) and prochymosin genes from calves, and plasmids contg. the genes which are capable of replicating in a prokaryotic organism. The prokaryotic organism is pref. an Escherichia species, esp. E. coli p Gx 1225 (NRRL B-15061). The microorganisms transformed by the plasmid are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial vector; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protolytic enzyme; zymogen; rennin; chymosin; cheese making;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN30022
                                                                                                                                                     Isolated chymosin or rennin and prochymosin genes - which replicate in prokaryotic organisms, esp. Esche and organisms used for chymosin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-NOV-1983.
Lactic acid proteinase;
                                  Cloned sequence of (pro)chymosin.
                                                                                                  AAN91157 standard; DNA; 1291 BP.
                                                                                                                                                                                                                                                       Sequence 1289 BP; 310 A; 391 C; 327 G;
                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 33-36; 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1983-820813/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1983;
                                                        07-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
bacteria;
pSK112; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               veal chymosin gene
                                                      (first entry)
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82US-0394433
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1..1140
/*tag= a
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            cheese; Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                 Score 49; DB 4; L
Pred. No. 1.4e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                        260 T; 1 other;
            cremoris
                                                                                                                                                                                                                                                                                                                                                                            nes - plasmid(s)
Escherichia coli,
                                                                                                                                                                                                                        Length 1289;
                                                                                                                                                                                                   Indels
            SK112; chymosin;
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                                                                                                                                                                                                   Gaps
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Qy
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                                                                                       Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                The DNA encoding prochymosin can be cloned into a plasmid (esp. from S. cremor1s SK112) and used to produce large amts of the protein by recombinant DNA techniques. This could overcome the shortage of prochymosin due to shortage of calf stomachs and increasing cheese prodn. Prochymosin is also used in prodn. of yoghurt, butter and buttermilk. See also AAN91158-N91160.
                                         DNA fragment is contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor_RNA
                                                                                                                                             Sequence 1291 BP;
                                                                                                                                                                                                                                              Disclosure; fig 2; 43pp; Dutch.
                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                WPI; 1989-030097/04.
P-PSDB; AAP94144.
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                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NL8701378-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                  t having region specific for lactic acid bacteria d in plasmid in microorganism used in prodn. of food prodn. eg cheese.
                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 29..1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=;prochymosin
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                                                                                                                                              323 A;
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2002, 01:58:17
                                                                                                                                              385 C; 326 G;
                                                                                       Score 49; DB 10; I
Pred. No. 1.4e-11;
0; Mismatches 0;
                                                                                                                                               257 T; 0 other;
                                                                                                             Length 1291;
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Search completed: August 1, 2002, 01:58:17 Job time: 16992 sec

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Title:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AV439574	AV542531	AV532027	AZ457432	AV555646	A2107068	AV557282	AV548208	AV518638	AI479358	AV536021	AQ711285	AA411566	AV559941	AV518232	AQ192651	AA411567	AA969042	AV538262	T20903	AV532492	вн261085	AQ907383	BB489847	BB493759	AU073299	BI974502	BG399700
_	AV542531 AV542531	AV532027 AV532027	AZ457432 1M0260F18	AV555646 AV555646	AZ107068 RPCI-23-2					AV536021 AV536021	t n	AA411566 zv22g01.r		AV518232 AV518232	_		AA969042 op43d07.s	AV538262 AV538262	N	AV532492 AV532492		AQ907383 GSSTc0941		вв493759 вв493759	AU073299 AU073299	BI974502 sai69d07.	BG399700 602441568

## ALIGNMENTS

FEATURES SOUTCE			REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG938086 LOCUS DEFINITION
Location/Qualifiers 1. 383 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="Boyine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)"	E-value of 0.0  PCR PRimers FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 383 POLYA-No.	Beef Genonics Laboratory  Dept of AFNS, University of Alberta  410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  Tel: 780 492 0169  Fax: 780 492 4265  Email: smoor@eafns.ualberta.ca  The sequence best matches 9b:BPU19786 (Bos primigenius prochymosin  The sequence best matches 9b:BPU19786 (Bos primigenius prochymosin	1 (bases 1 to 383) 1 (bases 1 to 383) Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G. CDNA's from bovine abomasum tissue Unpublished (2001) Contact: Dr. Stephen Moore	BG938086.1 GI:14337458 EST. cow. Bos taurus Eukaryota; Metazoa; Chordată; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bos taurus	BG938086 383 bp mRNA linear EST 11-JUN-2001 1AbollA08 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA

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RESULT
BG937697
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AUTHORS
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  52
TGTTCTCGGTTTACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCT 106
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                                                                                                        L Similarity
49; Conserv
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High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore,S.S., Hansen,C., Li,C.,
CDNA's from bovine abomasum ti
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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                                                                                                     1.2%; Sillarity 100.0%; Conservative 0;
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/lab_host="%XL1-BlueMRF'.strain"
/note="Organ: Abomasum; Vector: Uni-2%APXR; Site_1: EcoR
I; Site_2: Xho I"
a 111 c 113 g 76 t
                                                                                                                                                                                                                                                                /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
I; Office and the strain adult adult and the strain adult adult adult and the strain adult adu
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Bovine Abomasum cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                 cell_type="Epithelial"
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3. 2.5e-08;
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1Abo15E12
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49; Conserv
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                       BG937723 399 bp mRNA labou5D06 Bovine Abomasum cDNA Library Bos
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High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVCHYMOA (bovine chymosin a (rennin)
mrna) in main database at high score of 928.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 472)
Moore, S.S., Hansen, C., Li, C., Fu, A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec Bovidae; Bovinae; Bos.
1 (bases 1 to 399)
                                                            Bos taurus
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Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Young adult"
/lab_host="xil-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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Bovine Abomasum cDNA Library
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Pred. No.
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                                               eostomi;
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JOURNAL
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                                                                                                                                                                                                         Developmental cDNA in Dictyostelium discoideum (1999) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                 AU073125 240 bp mRNA linear EST 24-JUN-199 AU073125 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA cione SSG202, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore, S.S., Hansen, C., Li,C., Fu,A., Meng,Y. and Li,G. cDNA's from bovine abomasum tissue Unpublished (2001) Contact: Dr. Stephen Moore
                                                                                                                                                                                          Contact: Hideko Urushihara
                                                                                                                                                                                                                                          Urushihara, H.
                                                                                                                                                                                                                                                                                      Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dept of AFNS, University of Alberta
410 Agr1/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                        University of Tsukuba
                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                      AU073125.1 GI:5179546
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Seq primer: T3 primer
                                                                                                                                                                        Institute of Biological Sciences
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E-value of 0.0
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sequence best matches gb.BPU19786 (Bos primigenius prochymosin
A, complete cds)in main database at high score of 767.0 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Sillarity 100.0%; Conservative 0;
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                                                                                                        Ten-nodai, Tsukuba, Ibaraki 305, Japan d402hu@sakura.cc.tsukuba.ac.jp T - Dictyostelium discoideum cDNA project
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SSG202"
/clone_lib="Dictyostelium discoideum SS
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                             Location/Qualifiers
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/lab_host="XL1-BlueMRF'-strain"
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121 c 112 g
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   (H.Urushihara)"
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AA394733
AA394733.1
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lansing, Mi
Tel: 517-353-0854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: 22313tcn@ibm.cl.msu.edu
Seq primer: M13 -21 dye primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. and Somerville, C.
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/Clone_lib="Lambda-PRL2"
//Clone_lib="Lambda-PRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Note Zib-Lox; Site_2: No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="163F20XP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No.
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AG091550/c
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AG091550
AG09155.1 GI:16643352
GSS; GSS (genome survey sequestions)
Pan troglodytes male lymphologytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi.ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG091550
1 (bases 1 to 136)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RC1-NT0033-090800-016-a01 NT0033
                                                                                      Mammalia; Eutheria;
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                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
166 c 130 g 236 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="PTB-091H03.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No.
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36;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rdax: 15.5 ft 2000 to the FAPESP/LICR Human Cancer Genome This sequence was derived from the FAPESP/LICR Human Cancer Genome This sequence was derived from the following URL This sequence was derived from the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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Seq primer: puc 18 forward
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                   Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
                                                                                                                                                                                    Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage o
                                                                                                                                                                                                                                                                                                                                                                               EST
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99156227
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                                                                                                      Contact: Hideko Urushihara
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                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
PROJECT =
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quality sequence stop: 136.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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'Dictyostelium discoideum
                                                                                                                                             (6), 335-340 (1998)
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. 2.3e+02;
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(H.Urushihara) Dictyostelium
  cDNA project
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RESULT 11
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                      AA441444
LD16384.5prime LD Drosophila
Drosophila melanogaster cDNA
AA441444
AA441444.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU053870 312 bp mRNA linear
AU053870 Dictyostelium discoideum SL (H.Urushihara)
discoideum cDNA clone SLJ838, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Hideko Urushihara
Institute of Biological Sciences
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AU053870
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I = Dictyostelium discoideum
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SLA138"
/clone="SLA138"
/clone_lib="Dictyostelium discoideum S
/dev_stage="slug"
/dev_stage="slug"
/a 32 c 28 g 72 t
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/dev_stage="slug"
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/clone="SLJ838"
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/strain="AX4"
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                      bp mRNA linear EST 19-APR-2001
melanogaster embryo BlueScript
clone LD16384 5prime, mRNA sequence.
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1.7e+02;
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Fax: 510 486 6798
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3404 taaaataataataataataaata 3427
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 442)
Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang
                                                                                                                                                                                                                                                            Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yos
Yoshino,R., Mitta,B.N., Pi,M., Sato,T., Takemoto,K., Yasuka
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
Developmental CDNA in Dictyostelium discoideum
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500 bp mRNA linear EST 28-APR-19-AU052887 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLF272, mRNA sequence.
                                                                            Email: d402hu@sakura.cc.tsukuba.ac
PROJECT = Dictyostelium discoideum
                                                                                                                           3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum.
Dictyostelium discoideum
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Location/Qualifiers
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BDGP/HMI Drosophila EST Project
Unpublished (2001)
On Jun 2, 1997 this sequence very
                                                                                                                                                         University of Tsukuba
                                                                                                                                                                               Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
1 (bases 1 to 500)
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Plate: 163 row: G column: 12
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One Cyclotron Rd, Berkeley, CA
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Conservative 0;
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89 c 94 g 83 t
                                                    Location/Qualifiers
/organism="Dictyostelium discoideum"
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
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/db_xref="BDGP_EST:BDcln015599"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Olong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-204G22.TV
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   24;
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                                                                                                                                                                                                                                                                                                                                                               (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 204 row: G column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat
                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                 Seq primer: SP6
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llarity 100.0%;
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                                                                                                       Pieter de Jong"
1 103 c 89
                                                                                                                                         /note="Vector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
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                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                           /cell_type="Brain"
                                                                                                                                                                                             /sex="Female"
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Pred. No.
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   ore 24; DB 12;
Pred. No. 98;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbeëtigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seg primer: T?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Shaying Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602793535F1 NCI_CGAP_SG2
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1 (bases 1 to 667)
                                BG872501.1 GI:14223041
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                                                                              mRNA sequence.
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                 house mouse
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   musculus
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                                                                                                                                                                                                                                                     0.6%; S ilarity 100.0%; Conservative 0;
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RPCIII Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
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                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10848 row: e column: 09
High quality sequence stop: 655.
Location/Qualifiers
1 700
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                               0.6%; Score 24; DB ilarity 100.0%; Pred. No. 85 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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a 149 c 152 g 181 t
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